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Range: from begin to end Features: ☒ CDD

☐ 1: [XP\\_001502439](#). Reports PREDICTED: simila...[gi:149705828]

[BLink](#), [Conserved Domains](#), [Links](#)

[Comment](#) [Features](#) [Sequence](#)

**LOCUS** XP\_001502439 481 aa linear MAM 25-JUN-2007  
**DEFINITION** PREDICTED: similar to Hyaluronoglucosaminidase 4 [Equus caballus].  
**ACCESSION** XP\_001502439  
**VERSION** XP\_001502439.1 GI:149705828  
**DBSOURCE** REFSEQ: accession [XM\\_001502389.1](#)  
**KEYWORDS** .  
**SOURCE** Equus caballus (horse)  
**ORGANISM** [Equus caballus](#)  
**COMMENT** [MODEL REFSEQ](#): This record is predicted by automated computational analysis. This record is derived from an annotated genomic sequence ([NW\\_001799716](#)) using gene prediction method: GNOMON, supported by mRNA evidence.  
 Also see:

[Documentation](#) of NCBI's Annotation Process

**FEATURES** Location/Qualifiers  
**source** 1..481  
 /organism="Equus caballus"  
 /isolate="Twilight"  
 /db\_xref="taxon:9796"  
 /chromosome="4"  
 /sex="female"  
 /breed="thoroughbred"  
**[Protein](#)** 1..481  
 /product="similar to Hyaluronoglucosaminidase 4"  
 /calculated\_mol\_wt=54569  
**[Region](#)** 41..373  
 /region\_name="Glyco\_hydro\_56"  
 /note="Hyaluronidase; pfam01630"  
 /db\_xref="CDD:89585"  
**[CDS](#)** 1..481  
 /gene="LOC100056514"  
 /coded\_by="XM\_001502389.1:72..1517"  
 /db\_xref="GeneID:100056514"

**ORIGIN**

```

1 mkl1segqfr fcvvqpihlt swlliffilk sisslkparl piyqrkpfia awnaptqcl
61 ikynirlnlk mfvqigspla kargqnvtf yvnrlgyypw ytsqgvpvng glpqnislgv
121 hlekadedin yyipaedfsg lavidweywr pqwarnwntk dvyqrksrkl isdmqenvsa
181 tdieylakak feesakafmk etielgiks pklwgyyly pdchnynvyd pnytgscpee
241 evlrnnelsw lwnssaaly p sigvrkslgs senilrfsqf rvhesmrst mtshdyalpv
301 fvytrlygyrd eplflfslkqd listigesaa lgaagfviwg dmnltssegn ctkvkqfvss
361 vlrgyivnvt raaeacslhl crnngrcclr vwkapydlhl npasyyieas edgefivvegk
    
```

421 asdtdlalma ekfscqcyqg yegadcremk tadgcsghps fsgslitlcp lflagyqsiq  
481 1

//

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Exhibit B



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Search Protein for

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Range: from begin to end

Features: ☒ CDD ☐ 1: [AAC98883](#). Reports hyaluronidase 4 [...[gi:4090792](#)][BLink](#), [Conserved](#)[Domains](#), [Links](#)[Features](#) [Sequence](#)

LOCUS AAC98883 481 aa linear PRI 14-OCT-1999  
 DEFINITION hyaluronidase 4 [Homo sapiens].  
 ACCESSION AAC98883  
 VERSION AAC98883.1 GI:4090792  
 DBSOURCE locus AF009010 accession [AF009010.1](#)  
 KEYWORDS  
 SOURCE  
 ORGANISM [Homo sapiens](#)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
 Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (residues 1 to 481)  
 AUTHORS Csoka,A.B., Scherer,S.W. and Stern,R.  
 TITLE Expression analysis of six paralogous human hyaluronidase genes  
 clustered on chromosomes 3p21 and 7q31  
 JOURNAL Genomics 60 (3), 356-361 (1999)  
 PUBMED [10493834](#)  
 REFERENCE 2 (residues 1 to 481)  
 AUTHORS Csoka,A.B.  
 TITLE Direct Submission  
 JOURNAL Submitted (17-JUN-1997) Pathology, University of California,  
 Parnassus at 3rd Avenue, San Francisco, CA 94143, USA  
 COMMENT Method: conceptual translation supplied by author.  
 FEATURES  
 source  
 1..481  
 /organism="Homo sapiens"  
 /db\_xref="taxon:[9606](#)"  
 /chromosome="7"  
 /map="7q31.3"  
[Protein](#)  
 1..481  
 /product="hyaluronidase 4"  
 /name="PH-20 paralog"  
[Region](#)  
 41..373  
 /region\_name="Glyco\_hydro\_56"  
 /note="Hyaluronidase; pfam01630"  
 /db\_xref="CDD:[89585](#)"  
[CDS](#)  
 1..481  
 /gene="HYAL4"  
 /coded\_by="AF009010.1:642..2087"  
 /note="highest expression in placenta and skeletal muscle"  
 ORIGIN  
 1 mkvlsegqlk lcqvqpvlht swlliffilk siscclkparl piyrqkpfia awnaptdqcl  
 61 ikynlrlnlk mfpvigspla kargqnvtf yvnrlgyypw ytsqgyping glpqnislqv  
 121 hlekadqdin yyipaedfsg laavidweywr pqwarnwnsk dvyrqksrkl isdmgnknsa

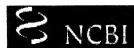
181 tdieylakvt feesakafmk etiklgiksr pkglgwgyly pdchnynvya pnysgscped  
241 evlrnnelsw lwnssaalyp sicvwksld senilrfskf rvhesmrist mtshdyalpv  
301 fvytrlgyrd eplfflskqd lvstigesaa lgaagiviwg dmnltaskan ctkvkqfvss  
361 dlgsyianvt raaevcs1hl crnngrcirk mwnapsylhl npasyhieas edgeftvkqk  
421 asdtdlavma dtfschcyqg yegadcreik tadgcsqvsp spgslmtlcl lllasyrsiq  
481 1

//

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Exhibit C



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to end

Features: ☒ CDD

+

☐ 1: [XP\\_001086758](#). Reports PREDICTED: simila...[gi:109068040]BLink, Conserved  
Domains, Links[Comment](#) [Features](#) [Sequence](#)

LOCUS XP\_001086758 481 aa linear PRI 14-JUN-2006

DEFINITION PREDICTED: similar to hyaluronoglucosaminidase 4 [Macaca mulatta].

ACCESSION XP\_001086758

VERSION XP\_001086758.1 GI:109068040

DBSOURCE REFSEQ: accession [XM\\_001086758.1](#)

KEYWORDS

SOURCE Macaca mulatta (rhesus monkey)

ORGANISM [Macaca mulatta](#)Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.COMMENT MODEL REFSEQ: This record is predicted by automated computational  
analysis. This record is derived from an annotated genomic sequence  
([NW\\_001114282](#)) using gene prediction method: GNOMON, supported by  
mRNA and EST evidence.

Also see:

[Documentation](#) of NCBI's Annotation Process

## FEATURES

source

Location/Qualifiers

1..481

/organism="Macaca mulatta"

/isolate="17573"

/db\_xref="taxon:9544"

/chromosome="3"

/sex="female"

/country="USA: Southwest National Primate Research Center  
at the Southwest Foundation for Biomedical Research, San  
Antonio, TX"

/note="derived from Indian origin rhesus"

[Protein](#)

1..481

/product="similar to hyaluronoglucosaminidase 4"

/calculated\_mol\_wt=54446

[Region](#)

41..373

/region\_name="Glyco\_hydro\_56"

/note="Hyaluronidase; pfam01630"

/db\_xref="CDD:89585"

[CDS](#)

1..481

/gene="LOC696128"

/coded\_by="XM\_001086758.1:54..1499"

/db\_xref="GeneID:696128"

## ORIGIN

```

1  mkvlpegqlr lcfvpvhl tllliffilk sisclpklr piyqrkpfia awnaptdqcl
61 ikynlrlnlk mfpvigspla kargqnvtf yvnrlgyypv ytsqgvping glpqnsislqv
121 hlekadqdin yyipdedfsg laavidweywr pqwarnwnak dvyrkksskl itdmgnknsa

```



```
181 tdieylakvt feesakafmk etiklgiksr pkglwgyly pdchnynvya pnytgscpee
241 evlrnnelsw lwnssaalyp sigvwksld senilrfsqf rvhesmrist mtshdyalpv
301 fvytrlgyrd epflflskqd lvstigesaa lgaagiviwg dmltsskan ctkvkqfvss
361 dlgsylanvt raaevcsfhl crnngrcirk mwnsptylhl npasyhieas edgeftvkgr
421 asdtdlavma dtfschcyqg yegadcrevk tadgcsqvsp fpgslitlcl lllasyrsih
481 1
```

//

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Exhibit D

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Range: from [begin](#) to [end](#) Features: ☒ CDD [+](#) [Refresh](#)

☐ 1: NP\_084124. Reports hyaluronoglucosam...[gi:116812879]

[BLink](#), [Conserved Domains](#), [Links](#)

[Comment](#) [Features](#) [Sequence](#)

LOCUS NP\_084124 481 aa linear ROD 11-FEB-2008  
 DEFINITION hyaluronoglucosaminidase 4 [Mus musculus].  
 ACCESSION NP\_084124 XP\_132998 XP\_917828 XP\_995969  
 VERSION NP\_084124.1 GI:116812879  
 DBSOURCE REFSEQ: accession [NM\\_029848.1](#)  
 KEYWORDS .  
 SOURCE Mus musculus (house mouse)  
 ORGANISM [Mus musculus](#)  
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
     Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
     Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 REFERENCE 1 (residues 1 to 481)  
 AUTHORS Kim,E., Baba,D., Kimura,M., Yamashita,M., Kashiwabara,S. and Baba,T.  
 TITLE Identification of a hyaluronidase, Hyal5, involved in penetration of mouse sperm through cumulus mass  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 102 (50), 18028-18033 (2005)  
 PUBMED [16330764](#)  
 REFERENCE 2 (residues 1 to 481)  
 AUTHORS Zhang,H., Shertok,S., Miller,K., Taylor,L. and Martin-Deleon,P.A.  
 TITLE Sperm dysfunction in the Rb(6.16)- and Rb(6.15)-bearing mice revisited: involvement of Hyalpl and Hyal5  
 JOURNAL Mol. Reprod. Dev. 72 (3), 404-410 (2005)  
 PUBMED [16078272](#)  
 COMMENT PROVISIONAL [REFSEQ](#): This record has not yet been subject to final NCBI review. The reference sequence was derived from [BC125402.1](#). On or before Oct 30, 2006 this sequence version replaced [gi:20915092](#), [gi:82802536](#), [gi:94378449](#).  
 FEATURES  
     source Location/Qualifiers  
         1..481  
         /organism="Mus musculus"  
         /db\_xref="taxon:10090"  
         /chromosome="6"  
     Protein 1..481  
         /product="hyaluronoglucosaminidase 4"  
         /calculated\_mol\_wt=54254  
     Region 41..373  
         /region\_name="Glyco\_hydro\_56"  
         /note="Hyaluronidase; pfam01630"  
         /db\_xref="CDD:89585"  
     CDS 1..481  
         /gene="Hyal4"  
         /coded\_by="NM\_029848.1:218..1663"  
         /db\_xref="CCDS:CCDS39441.1"

/db\_xref="GeneID:77042"

/db\_xref="MGI:1924292"

## ORIGIN

```
1 mqlpegqlr lcvfqpvhlt sgllilfilk sisslkparl pvyqrkpfia awnaptdlcl
61 ikynltlnlk vfgmqvgsprl kdrqgnvif yanrlgyypw ytsegvping glpqntslqv
121 hlkkaaqdin yyipsenfsg laavidweywr pqwarnwntk diyqrksrtl isdmkenisa
181 adieysakat feksakafme etiklgsksr pkglwgyyly pdchnynvya tnytgsctpee
241 evlrnndls wnsstaly p avsirksfad sentlhfsrf rvreslrist mtsqdyalpv
301 fvytqlgyke eplflskqd listigesaa lgaagivvwg dmnltssseen ctkvnrfvns
361 dfgsyiinv raaevcsrhl cknngrcvrk twkaahylhl npasyhieas edgefivrgr
421 asdtdlavma enflchcyeg yegadcremt easgpgslsl ssssvitlcl lvmagysiq
481 1
```

//

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Exhibit E



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Range: from begin to end

Features: ☒ CDD [+](#)[Refresh](#)☐ 1: [XP\\_527872](#). Reports PREDICTED: hyalur...[gi:114615742][Blink, Conserved](#)[Domains, Links](#)[Comment](#) [Features](#) [Sequence](#)

LOCUS XP\_527872 476 aa linear PRI 15-SEP-2006

DEFINITION PREDICTED: hyaluronoglucosaminidase 4 [Pan troglodytes].

ACCESSION XP\_527872

VERSION XP\_527872.2 GI:114615742

DBSOURCE REFSEQ: accession [XM\\_527872.2](#)

KEYWORDS

SOURCE Pan troglodytes (chimpanzee)

ORGANISM [Pan troglodytes](#)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Pan.

COMMENT MODEL REFSEQ: This record is predicted by automated computational analysis. This record is derived from an annotated genomic sequence ([NW\\_001238093](#)) using gene prediction method: GNOMON, supported by mRNA and EST evidence.

Also see:

[Documentation of NCBI's Annotation Process](#)On Sep 15, 2006 this sequence version replaced gi:[55629380](#).

FEATURES

source

Location/Qualifiers

1..476

/organism="Pan troglodytes"

/isolate="Yerkes chimp pedigree #C0471 (Clint)"

/db\_xref="taxon:[9598](#)"

/chromosome="7"

/sex="male"

[Protein](#)

1..476

/product="hyaluronoglucosaminidase 4"

/calculated\_mol\_wt=53658

[Region](#)

41..373

/region\_name="Glyco\_hydro\_56"

/note="Hyaluronidase; pfam01630"

/db\_xref="CDD:[89585](#)"[CDS](#)

1..476

/gene="HYAL4"

/coded\_by="XM\_527872.2:634..2064"

/db\_xref="GeneID:[472497](#)"

ORIGIN

```

1 mkvlserqlk lcvqpvhlt swlliffilk sisclkarpl piyerkpfia awnaaptqcl
61 ikynlrlnlk mfpvigspla kargqhvtf yvnrlgyypw ytsqgvping glpqnislqv
121 hlekadqdin yyipaedfsg laavidweywr pgwarnwnak dvyrgksrkl isdmgnvsa
181 tdieylakvt feesakafmk etiklgiks pklwggyly pdchnynvya pnytgscpd
241 evlrnnelsw lwnssaalyp sigvkslsgd senilrfskf rvhesmrist mtshdyalpv
301 fvytrlglyrd eplflfskqd lvstigesaa lgaagiviwg dmlntsskan ctkvkqfvss

```




361 dlgsyianvt raaevcsllh crnngrcirk mwnapsylhl npasyhieas edgeftvkkgk  
421 asdtdlavma dtfschcygg yegadcreik tadgcsgvsp spgsimtlcl lllasy

//

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Exhibit F

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Range: from  begin to end 
 Features: ☒ CDD

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[BLink](#), [Conserved Domains](#), [Links](#)
[Comment](#)
[Features](#)
[Sequence](#)

**LOCUS** XP\_578235 481 aa linear ROD 22-JUN-2006  
**DEFINITION** PREDICTED: similar to hyaluronoglucosaminidase 4 [Rattus norvegicus].  
**ACCESSION** XP\_578235  
**VERSION** XP\_578235.1 GI:62647063  
**DBSOURCE** REFSEQ: accession [XM\\_578235.1](#)  
**KEYWORDS** .  
**SOURCE** Rattus norvegicus (Norway rat)  
**ORGANISM** [Rattus norvegicus](#)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.  
**COMMENT** **MODEL REFSEQ:** This record is predicted by automated computational analysis. This record is derived from an annotated genomic sequence ([NW\\_047689](#)) using gene prediction method: GNOMON, supported by mRNA evidence.  
 Also see:

[Documentation](#) of NCBI's Annotation Process

**FEATURES** Location/Qualifiers  
**source** 1..481  
 /organism="Rattus norvegicus"  
 /strain="BN/SsNHsdMCW"  
 /db\_xref="taxon:10116"  
 /chromosome="4"  
**Protein** 1..481  
 /product="similar to hyaluronoglucosaminidase 4"  
 /calculated\_mol\_wt=54180  
**Region** 41..373  
 /region\_name="Glyco\_hydro\_56"  
 /note="Hyaluronidase; pfam01630"  
 /db\_xref="CDD:89585"  
**CDS** 1..481  
 /gene="Hyal4"  
 /coded\_by="XM\_578235.1:1..1446"  
 /db\_xref="GeneID:404783"  
 /db\_xref="RGD:1303194"  
**ORIGIN**  
 1 mqllseggqlr rcvqvphlt sglliffilk sisslkparl pvyqrkpfia awnaptdlcl  
 61 ikynlavlntk vfmvgspri kdrqrnvif yanklgsypw ytseggvping glpqntsrlqv  
 121 hlekayqdin yyipnsenfsg laavidweywr pqwarnwnkt diyrqksrtl isdmkenist  
 181 adieylakata feksakafme etiklgiks pkgfwggyly pdchnynfya tnytgscpee  
 241 evlrnndlsu lwnsstalyp avsirksfad sentlhfsqf rvreslrist mtshdyalpv  
 301 fvtyrlgyke epllfiskqd listigesaa lgaagivvwg dmlntssaen ctkvnrfvns

```
361 dfgsyvint taaevcsrhl cknngrcark twkaahylhl npasyhieas adrefvvkgr
421 asdadlaama enflchcyeg yegadcrdmt easgpsgvsv ssssvitlcl ialaghqsiq
481 1
```

//

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Exhibit G



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Genome

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Range: from begin

to end

Features:

☒ CDD

+

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☐ 1: [XP\\_532444](#). Reports PREDICTED: simila...[gi:73975681]

BLink, Conserved

Domains, Links

Comment Features Sequence

LOCUS XP\_532444 481 aa linear MAM 30-AUG-2005

DEFINITION PREDICTED: similar to hyaluronoglucosaminidase 4 isoform 1 [Canis familiaris].

ACCESSION XP\_532444

VERSION XP\_532444.2 GI:73975681

DBSOURCE REFSEQ: accession [XM\\_532444.2](#)

KEYWORDS .

SOURCE Canis lupus familiaris (dog)

ORGANISM [Canis lupus familiaris](#)

COMMENT MODEL REFSEQ: This record is predicted by automated computational analysis. This record is derived from an annotated genomic sequence ([NW\\_876258](#)) using gene prediction method: GNOMON, supported by EST evidence. Also see:

Documentation of NCBI's Annotation ProcessOn Aug 30, 2005 this sequence version replaced [gi:57095952](#).

FEATURES

Location/Qualifiers

source

1..481

/organism="Canis lupus familiaris"

/sub\_species="familiaris"

/db\_xref="taxon:9615"

/chromosome="14"

/breed="boxer"

Protein

1..481

/product="similar to hyaluronoglucosaminidase 4 isoform 1"

/calculated\_mol\_wt=54487

Region

41..373

/region\_name="Glyco\_hydro\_56"

/note="Hyaluronidase; pfam01630"

/db\_xref="CDD:89585"

CDS

1..481

/gene="LOC475212"

/coded\_by="XM\_532444.2:1..1446"

/db\_xref="GeneID:475212"

ORIGIN

```

1  mkvlsdggqlr lcvvqpihlt swlliffilk sisslkparl piyqrkpfia awnaptdqcl
61  ikyniginlnk mfvqigspla kargqnitif yvnrlgyypw ytsqgvping glpqnislqv
121 hlekadqdin yyipaedfng lavidweywr pgwarnwntk dvyrgksrkl isdmqenvsa
181 tdieylakat feesakafmk etielgiks pklwgyyly pdchnynvya pnygtscpee
241 evlrnnelsw lwnssaalyp sigvrksled nenilrfsrf rvheslrist mtshdyalpi

```

```
301 fvytrlgyrn eplfflskqd listigesaa lgaagiviwg dmlttssegn ctkvkgyvss
361 dlghyivnvt raaevcs1hl crsngrcirk vwkapdylhl npasyhieas kdgefivkgk
421 asdmdleale ekfschcygg yegadcrgtk tadgcsgvfs fssslitlcl lvlagysir
481 s
```

//

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**BLAST Basic Local Alignment Search Tool****Job Title: lcl|791 (1271 letters)**

---

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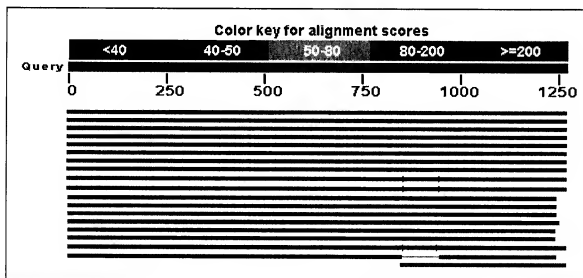
**BLASTN 2.2.18+**

RID: 62JPMG3G013 **Database:** All GenBank+EMBL+DBBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences) 6,953,186 sequences; 24,085,767,743 total letters

**Query=** Length=1271

**Distribution of 26 Blast Hits on the Query Sequence**

---



Distance tree of results **NEW**Legend for links to other resources: **U** UniGene **E** GEO **G** Gene **S** Structure **N****Sequences producing significant alignments:**

(Click headers to sort columns)

<b>NM_012269.2</b>	Homo sapiens hyaluronoglucosaminidase 4 (HYAL4), mRNA	2348	2348	100%	0.0	100%	<b>UG</b>
<b>BC104790.1</b>	Homo sapiens hyaluronoglucosaminidase 4, mRNA (cDNA clone MGC:132450 IMAGE:8143793), complete cds	2342	2342	100%	0.0	99%	<b>UG</b>
<b>BC104788.1</b>	Homo sapiens hyaluronoglucosaminidase 4, mRNA (cDNA clone MGC:132448 IMAGE:8143791), complete cds	2342	2342	100%	0.0	99%	<b>UG</b>
<b>AF009010.1</b>	Homo sapiens hyaluronidase 4 (HYAL4) mRNA, complete cds	2331	2331	100%	0.0	99%	<b>UE</b> <b>G</b>
<b>XM_527872.2</b>	PREDICTED: Pan troglodytes hyaluronoglucosaminidase 4 (HYAL4), mRNA	2287	2287	100%	0.0	99%	<b>G</b>
<b>XM_001086758.1</b>	PREDICTED: Macaca mulatta similar to hyaluronoglucosaminidase 4 (LOC696128), mRNA	2154	2154	100%	0.0	97%	<b>G</b>
<b>XM_001502389.1</b>	PREDICTED: Equus caballus similar to Hyaluronoglucosaminidase 4 (LOC100056514), mRNA	1742	1742	99%	0.0	91%	<b>G</b>
<b>XM_532444.2</b>	PREDICTED: Canis familiaris similar to hyaluronoglucosaminidase 4, transcript variant 1 (LOC475212), mRNA	1659	1659	99%	0.0	90%	<b>UE</b> <b>G</b>
<b>AC006029.2</b>	Homo sapiens BAC clone GS1-195F7 from 7q31.2-q32, complete sequence	1578	2359	100%	0.0	100%	
<b>AC197510.3</b>	Pan troglodytes BAC clone CH251-712N23 from chromosome 7, complete sequence	1539	2298	100%	0.0	99%	
<b>BC132096.1</b>	Mus musculus hyaluronoglucosaminidase 4, mRNA (cDNA clone MGC:163727 IMAGE:40130373), complete cds	1339	1339	97%	0.0	86%	<b>UG</b>
<b>NM_029848.1</b>	Mus musculus hyaluronoglucosaminidase 4 (Hyal4), mRNA >gb BC125402.1  Mus musculus hyaluronoglucosaminidase 4, mRNA (cDNA clone MGC:159105 IMAGE:40129917), complete cds	1339	1339	97%	0.0	86%	<b>UE</b> <b>G</b>
<b>AK014599.1</b>	Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4632428M18 product:similar to HYALURONIDASE 4 [Homo sapiens], full insert sequence	1306	1306	97%	0.0	85%	<b>UE</b> <b>G</b>
<b>XM_001370681.1</b>	PREDICTED: Monodelphis domestica similar to Hyaluronoglucosaminidase 4 (LOC100017029), mRNA	1232	1232	98%	0.0	84%	<b>G</b>
<b>XM_001062033.1</b>	PREDICTED: Rattus norvegicus hyaluronoglucosaminidase 4 (Hyal4), mRNA	1212	1212	97%	0.0	84%	<b>G</b>
<b>XM_578235.1</b>	PREDICTED: Rattus norvegicus hyaluronoglucosaminidase 4 (Hyal4), mRNA	1212	1212	97%	0.0	84%	<b>UG</b>
<b>CU467663.10</b>		1136	1632	99%	0.0	90%	



Pig DNA sequence from clone CH242-  
113A4 on chromosome 18, complete  
sequence

AC130215.3	Mus musculus BAC clone RP23-286E1 from 976 1230 90% 0.0 87% 6, complete sequence	
XM_854096.1	PREDICTED: Canis familiaris similar to 475 475 33% 2e- 87% hyaluronoglucosaminidase 4, transcript 130 variant 3 (LOC475212), mRNA	<b>U E</b> <b>G</b>

## Alignments

>ref|NM\_012269.2| **UG** Homo sapiens hyaluronoglucosaminidase 4 (HYAL4), mRNA  
Length=2411

GENE ID: 23553 **HYAL4** | hyaluronoglucosaminidase 4 [Homo sapiens]  
(10 or fewer PubMed links)

Score = 2348 bits (1271), Expect = 0.0  
Identities = 1271/1271 (100%), Gaps = 0/1271 (0%)  
Strand=Plus/Plus

Query	1	GTCTAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGGAAATG	60
Sbjct	739	GTCTAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGGAAATG	798
Query	61	CTCCAACAGATCAGTGTGATATAAATAAATTTAAGACTAAATTTGAAAATGTTTCCTG	120
Sbjct	799	CTCCAACAGATCAGTGTGATATAAATAAATTTAAGACTAAATTTGAAAATGTTTCCTG	858
Query	121	TGATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAAATGTCATATATTTATGTCAACA	180
Sbjct	859	TGATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAAATGTCATATATTTATGTCAACA	918
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Sbjct	919	GATTGGGATACATCTCCGTGGTATACATCACAAGGGTCCCATTAATGGAGGTCTCCAC	978
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Sbjct	979	AGAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACATCC	1038
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Sbjct	1039	CTGCTGAAGATTTCAAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGTGGG	1098
Query	361	CCCGGAATCGAACTCAAAGAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCGATA	420
Sbjct	1099	CCCGGAATCGAACTCAAAGAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCGATA	1158
Query	421	TGGGAAAGAAATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAGAAA	480
Sbjct	1159	TGGGAAAGAAATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAGAAA	1218
Query	481	GTGCAAAAGCTTTTCATGAAGGAAACCATCAAATGGGAATTAAGAGCCGACCCAAAGGCC	540
Sbjct	1219	GTGCAAAAGCTTTTCATGAAGGAAACCATCAAATGGGAATTAAGAGCCGACCCAAAGGCC	1278
Query	541	TTTGGGGTTATTATTATATCTGATTGCCACAATTTATAAGCTTTATGCCCCAAACTACT	600
Sbjct	1279	TTTGGGGTTATTATTATATCTGATTGCCACAATTTATAAGCTTTATGCCCCAAACTACT	1338
Query	601	CTGGGTCATGCCAGAGACGAAGTCTTGAGGAACAATGAGCTCTCTGGCTCTGGAACA	660
Sbjct	1339	CTGGGTCATGCCAGAGACGAAGTCTTGAGGAACAATGAGCTCTCTGGCTCTGGAACA	1398
Query	661	GCAGTGCTGCTTTATATCTCTTATCGGTGTCTGGAATCCCTTGGAGACAGTGAAAAACA	720
Sbjct	1399	GCAGTGCTGCTTTATATCTCTTATCGGTGTCTGGAATCCCTTGGAGACAGTGAAAAACA	1458
Query	721	TTTTGCGCTTCTCCAAATTTTCGGGTGCATGAATCCATGAGGATCTCCACCATGACATCTC	780
Sbjct	1459	TTTTGCGCTTCTCCAAATTTTCGGGTGCATGAATCCATGAGGATCTCCACCATGACATCTC	1518
Query	781	ATGATTATGCTCTGCTGTTATTTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTTAT	840
Sbjct	1519	ATGATTATGCTCTGCTGTTATTTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTTAT	1578
Query	841	TTTTCTTTCTTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCTGCCTTGGGAGCTG	900

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Sbjct 1579 TTTTCCTTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAAGTGTCTGCCCTGGGGAGCTG 1638
Query 901 CAGGCATTGTTATTATTGGGGAGACATGAATTTAACTGCATCCAAGGCCAACTGTACAAAAGG 960
Sbjct 1639 CAGGCATTGTTATTATTGGGGAGACATGAATTTAACTGCATCCAAGGCCAACTGTACAAAAGG 1698
Query 961 TGAAGCAGTTTGTGAGTTCCTGATTTAGGGAGCTACATAGCCAAATGTGACCAGAGCTGCTG 1020
Sbjct 1699 TGAAGCAGTTTGTGAGTTCCTGATTTAGGGAGCTACATAGCCAAATGTGACCAGAGCTGCTG 1758
Query 1021 AGGTATGCAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCATAAGGAAGATGTGGAACG 1080
Sbjct 1759 AGGTATGCAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCATAAGGAAGATGTGGAACG 1818
Query 1081 CGCCCACTTACCTTCACCTTGAACCCCTGCAAGTTACACATAGAGGCCCTCTGAGGACGGGG 1140
Sbjct 1819 CGCCCACTTACCTTCACCTTGAACCCCTGCAAGTTACACATAGAGGCCCTCTGAGGACGGGG 1878
Query 1141 AGTTTACTGTGAAAGGAAAAGCATCTGATACAGACCTGGCAGTGATGGCAGATACATTTT 1200
Sbjct 1879 AGTTTACTGTGAAAGGAAAAGCATCTGATACAGACCTGGCAGTGATGGCAGATACATTTT 1938
Query 1201 CCTGTCAATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAATAAGACGCGCTGATG 1260
Sbjct 1939 CCTGTCAATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAATAAGACGCGCTGATG 1998
Query 1261 GCTGCTCTGGG 1271
Sbjct 1999 GCTGCTCTGGG 2009

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>gb|BC104790.1| **UG** Homo sapiens hyaluronoglucosaminidase 4, mRNA (cDNA clone MG IMAGE:8143793), complete cds  
Length=1552

GENE ID: 23553 **HYAL4** | hyaluronoglucosaminidase 4 [Homo sapiens]  
(10 or fewer PubMed links)

Score = 2342 bits (1268), Expect = 0.0  
Identities = 1270/1271 (99%), Gaps = 0/1271 (0%)  
Strand=Plus/plus

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Query 1 GTCTAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGGAAATG 60
Sbjct 177 GTCTAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGGAAATG 236
Query 61 CTCCAACAGATCAGTGTTTGATAAAATATAATTTAAGACTAAATTTGAAATGTTTCTCTG 120
Sbjct 237 CTCCAACAGATCAGTGTTTGATAAAATATAATTTAAGACTAAATTTGAAATGTTTCTCTG 296
Query 121 TGATTGGAAGCCCACTGGCCAAAGGCCAGGGGGCAAAATGTCACTATATTTTATGTCACAA 180
Sbjct 297 TGATTGGAAGCCCACTGGCCAAAGGCCAGGGGGCAAAATGTCACTATATTTTATGTCACAA 356
Query 181 GATTGGGATACTATCCGTGGTATACATCAAGGGGTCCCCATTAAATGGAGGTCTCCAC 240
Sbjct 357 GATTGGGATACTATCCGTGGTATACATCAAGGGGTCCCCATTAAATGGAGGTCTCCAC 416
Query 241 AGAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACATCC 300
Sbjct 417 AGAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACATCC 476
Query 301 CTGCTGAAGATTTTCAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGTGGG 360
Sbjct 477 CTGCTGAAGATTTTCAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGTGGG 536
Query 361 CCCGGAACTGGAACCTCAAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCGGATA 420
Sbjct 537 CCCGGAACTGGAACCTCAAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCGGATA 596
Query 421 TGGGAAAGAAATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAGAAA 480
Sbjct 597 TGGGAAAGAAATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAGAAA 656

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Query 481 GTGCAAAAGCTTTCATGAAGGAAACCATCAAATTGGGAATTAAAGAGCCGACCCAAAGGCC 540
Sbjct 657 GTGCAAAAGCTTTCATGAAGGAAACCATCAAATTGGGAATTAAAGAGCCGACCCAAAGGCC 716

Query 541 TTTGGGGTTATTATTTATATCTGATTGCCACAATTATAACGTTTATGCCCCAAACTACT 600
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Query 601 CTGGGTCATGCCCAGAAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTGGAACA 660
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Query 661 GCAGTGTCTGCTTTATATCTCTCTATCGGTGTCTGGAATCCCTTGGAGACAGTGAAGAAC 720
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Sbjct 897 TTTTGCAGCTTCTCCAAATTTCCGGTGCAATGATCCATGAGGATCTCCACCATGACATCTC 956

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Sbjct 1017 TTTTCCCTTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCTGCCTTGGGAGCTG 1076

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Query 961 TGAAGCAGTTTGTGAGTCTGATTAGGGAGCTACATAGCCAATGTGACCAGAGCTGCTG 1020
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Query 1021 AGGTATGCAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCATAAGGAAGATGTGGAACG 1080
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Query 1081 CGCCCGATTACCTTCACTTGAACCTGCAAGTTACCACATAGAGGCCTCTGAGGACGGGG 1140
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Query 1141 AGTTTACTGTGAAGGAAAAAGCATCTGATACAGACCTGGCAGTGATGGCAGATACATTTT 1200
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Query 1201 CCTGTCAATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAATAAAGACGGCTGATG 1260
Sbjct 1377 CCTGTCAATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAATAAAGACGGCTGATG 1436

Query 1261 GCTGCTCTGGG 1271
Sbjct 1437 GCTGCTCTGGG 1447

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>gb|BC104788.1| **UG** Homo sapiens hyaluronoglucosaminidase 4, mRNA (cDNA clone MG IMAGE:8143791), complete cds  
Length=1558

GENE ID: 23553 **HYAL4** | hyaluronoglucosaminidase 4 [Homo sapiens]  
(10 or fewer PubMed links)

Score = 2342 bits (1268), Expect = 0.0  
Identities = 1270/1271 (99%), Gaps = 0/1271 (0%)  
Strand=Plus/Plus

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Query 1 GTCTAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGGAAATG 60
Sbjct 177 GTCTAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGGAAATG 236

Query 61 CTCCAACAGATCAGTGTTTGTATAAAATATAAATTAAAGACTAAATTTGAAAAATGTTTCTCTG 120
Sbjct 237 CTCCAACAGATCAGTGTTTGTATAAAATATAAATTAAAGACTAAATTTGAAAAATGTTTCTCTG 296

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Query	121	TGATTGGAAGCCCACTG3CCAAGGCCAGGGGGCAAAATGTCACATATATTTTATGTCAACA	180
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Query	181	GATTGGGATACACTCCGTGGTATACATCACAGGGGTCCCCAATTAATGGAGGTCCTCCAC	240
Sbjct	357	GATTGGGATACACTCCGTGGTATACATCACAGGGGTCCCCAATTAATGGAGGTCCTCCAC	416
Query	241	AGAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACATCC	300
Sbjct	417	AGAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACATCC	476
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Sbjct	477	CTGCTGAAGATTTCAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGTGGG	536
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Sbjct	537	CCCGGAAGTGGAACTCAAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCGATA	596
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Sbjct	597	TGGGAAAGAAATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAGAAA	656
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Sbjct	777	CTGGGTCTGCCCAGAAGCGAAGTCTTGAGGAACAAATGAGCTCTCTTGGCTCTGGAACA	836
Query	661	GCAGTGCTGCTTTATATCCTTCTATCGGTGCTCGGAAATCCCTTGGAGACAGTGA AAAACA	720
Sbjct	837	GCAGTGCTGCTTTATATCCTTCTATCGGTGCTCGGAAATCCCTTGGAGACAGTGA AAAACA	896
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Sbjct	897	TTTTGCGCTTCTCCAAATTTCCGGTGTCATGAATCCATGAGGATCTCCACCATGACATCTC	956
Query	781	ATGATTATGCTCTGCCGTGATTTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTTAT	840
Sbjct	957	ATGATTATGCTCTGCCGTGATTTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTTAT	1016
Query	841	TTTTCTTTCTTAAGCAAGATCTAGTCAGCACCATTAGGAGAAAGTGCTGCCTTGGGAGCTG	900
Sbjct	1017	TTTTCTTTCTTAAGCAAGATCTAGTCAGCACCATTAGGAGAAAGTGCTGCCTTGGGAGCTG	1076
Query	901	CAGGCATTGTTATTTGGGGAGACATGAATTTAACTGCATCCAAGGCCAACTGTACAAAGG	960
Sbjct	1077	CAGGCATTGTTATTTGGGGAGACATGAATTTAACTGCATCCAAGGCCAACTGTACAAAGG	1136
Query	961	TGAAGCAGTTTGTGAGTTCTGATTTAGGGAGCTACATAGCCAATGTGACCAGAGCTGCTG	1020
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Query	1021	AGGTATGCAGCCTTCACCTCTGCAGGAACAAATGGCAGGTGCATAGGAAGATGTGGAAAG	1080
Sbjct	1197	AGGTATGCAGCCTTCACCTCTGCAGGAACAAATGGCAGGTGCATAGGAAGATGTGGAAAG	1256
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Sbjct	1257	CGCCAGTTACCTTCACTTGAACCCCTGCAAGTTACCACATAGAGGCCCTCTGAGGACGGGG	1316
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Sbjct	1317	AGTTTACTGTGAAGGAAAAAGCATCTGATACAGACCTGGCAGTGATGGCAGATACATTTT	1376
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Sbjct	1377	CCTGTCAATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAATAAGACGGCTGATG	1436

Query 1261 GCTGCTCTGGG 1271  
 Sbjct 1437 GCTGCTCTGGG 1447

>gb|AF009010.1|AF009010 **UEG** Homo sapiens hyaluronidase 4 (HYAL4) mRNA, complet  
 Length=2414

GENE ID: 23553 **HYAL4** | hyaluronoglucosaminidase 4 [Homo sapiens]  
 (10 or fewer PubMed links)

Score = 2331 bits (1262), Expect = 0.0  
 Identities = 1268/1271 (99%), Gaps = 0/1271 (0%)  
 Strand=Plus/Plus

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Sbjct	742	GCTCAAAACCTGCTCGACTTCCAATTTATCAAGGAAACCTTTTATAGCTGCTTGGAAATG	801
Query	61	CTCCAACAGATCAGTGTGTTGATAAAATATAATTTAAGACTAAATTTGAAAAATGTTTCCTG	120
Sbjct	802	CTCCAACAGATCAGTGTGTTGATAAAATATAATTTAAGACTAAATTTGAAAAATGTTTCCTG	861
Query	121	TGATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAATGTCACTATATTTTATGTCAACA	180
Sbjct	862	TGATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAATGTCACTATATTTTATGTCAACA	921
Query	181	GATTGGGATACATATCCGTGGTATACATCACAGGGGTCCCCATTAATGGAGGCTCCAC	240
Sbjct	922	GATTGGGATACATATCCGTGGTATACATCACAGGGGTCCCCATTAATGGAGGCTCCAC	981
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Sbjct	982	AGAACATAAGTTTACAAGTACATCTGGAAGAAAGCTGACCAAGATATTAATTATTACATCC	1041
Query	301	CTGCTGAAGATTTCAGTGGACTTGCTGTATAGATTGGGAATATTGGCGACCACAGTGGG	360
Sbjct	1042	CTGCTGAAGATTTCAGTGGACTTGCTGTATAGATTGGGAATATTGGAGACCACAGTGGG	1101
Query	361	CCCGGAACCTGGAACCTCAAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCGATA	420
Sbjct	1102	CCCGGAACCTGGAACCTCAAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCGATA	1161
Query	421	TGGGAAAGAAATGTATCAGCTACCGATATTGAATATTAGCCAAAGTGACCTTTGAAGAAA	480
Sbjct	1162	TGGGAAAGAAATGTATCAGCTACCGATATTGAATATTAGCCAAAGTGACCTTTGAAGAAA	1221
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Sbjct	1222	GTGCAAAAGCTTTTCATGAAGGAAACCATCAAATTTGGGAATTAAGAGCCGACCCAAAGGCC	1281
Query	541	TTTGGGGTTATTATTATATCTGATTGCCACAATTATAACGTTTATGGCCCAAACCTACT	600
Sbjct	1282	TTTGGGGTTATTATTATATCTGATTGCCACAATTATAACGTTTATGGCCCAAACCTACT	1341
Query	601	CTGGGTCATGCCAGAAGACGAAGCTTGAGGAACAATGAGCTCTCTTGGCTCTGGAACA	660
Sbjct	1342	CTGGGTCATGCCAGAAGACGAAGCTTGAGGAACAATGAGCTCTCTTGGCTCTGGAACA	1401
Query	661	GCAGTGCTGCTTTATATCTCTTATCGGTGCTTGGAAATCCCTTGGAGACAGTGAAAACA	720
Sbjct	1402	GCAGTGCTGCTTTATATCTCTTATCTGTCTTGGAAATCCCTTGGAGACAGTGAAAACA	1461
Query	721	TTTGGCGTTCTCCAAATTTTCGGGTGCATGAATCCATGAGGATCTCCACCATGACATCTC	780
Sbjct	1462	TTTGGCGTTCTCCAAATTTTCGGGTGCATGAATCCATGAGGATCTCCACCATGACATCTC	1521
Query	781	ATGATTATGCTCTGCGCTGATTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTTAT	840
Sbjct	1522	ATGATTATGCTCTGCGCTGATTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTTAT	1581
Query	841	TTTTCCTTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCTGCCTTGGAGCTG	900
Sbjct	1582	TTTTCCTTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCTGCCTTGGAGCTG	1641

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Query 901 CAGGCATTGTTATTTGGGGAGACATGAATTTAACTGCATCCAAGGCCAACTGTACAAAGG 960
Sbjct 1642 CAGGCATTGTTATTTGGGGAGACATGAATTTAACTGCATCCAAGGCCAACTGTACAAAGG 1701
Query 961 TGAAGCAGTTTGTGAGTTCGTAGTTTAGGGAGCTACATAGCCAAATGTGACCAGAGCTGCTG 1020
Sbjct 1702 TGAAGCAGTTTGTGAGTTCGTAGTTTAGGGAGCTACATAGCCAAATGTGACCAGAGCTGCTG 1761
Query 1021 AGGTATGCAAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCATAAGGAAGATGTGGAACG 1080
Sbjct 1762 AGGTATGCAAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCATAAGGAAGATGTGGAACG 1821
Query 1081 CGCCCAAGTTACCTTCACTTGAACCCCTGCAAGTTACACATAGAGGCCTCTGAGGACGGGG 1140
Sbjct 1822 CGCCCAAGTTACCTTCACTTGAACCCCTGCAAGTTACACATAGAGGCCTCTGAGGACGGGG 1881
Query 1141 AGTTTACTGTGAAAGGAAAAGCATCTGATACAGACCTGGCAGTGATGGCAGATACATTTT 1200
Sbjct 1882 AGTTTACTGTGAAAGGAAAAGCATCTGATACAGACCTGGCAGTGATGGCAGATACATTTT 1941
Query 1201 CCTGTCAATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAATAAGACGGCTGATG 1260
Sbjct 1942 CCTGTCAATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAATAAGACGGCTGATG 2001
Query 1261 GCTGCTCTGGG 1271
Sbjct 2002 GCTGCTCTGGG 2012

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>ref|XM\_527872.2| **G** PREDICTED: Pan troglodytes hyaluronoglucosaminidase 4 (HYAL4 mRNA)  
Length=2403

GENE ID: 472497 HYAL4 | hyaluronoglucosaminidase 4 [Pan troglodytes]

Score = 2287 bits (1238), Expect = 0.0  
Identities = 1261/1272 (99%), Gaps = 2/1272 (0%)  
Strand=Plus/Plus

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Query 1 GTCTAAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGTGTCTTGGAAATG 60
Sbjct 734 GTCTAAAACCTGCTCGACTTCCAATTTATGAAAGGAAACCTTTTATAGTGTCTTGGAAATG 793
Query 61 CTCCAACAGATCAGTGTTTGATAAAATATAATTTAAGACTAAATTTGAAAATGTTTCCTG 120
Sbjct 794 CTCCAACAGATCAGTGTTTGATAAAATATAATTTAAGACTAAATTTGAAAATGTTTCCTG 853
Query 121 TGATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAAATGTCACTATATTTTATGTCAACA 180
Sbjct 854 TGATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAACATGTCACTATATTTTATGTCAACA 913
Query 181 GATTGGGATACATATCCGTGGTATACATCACAAGGGGTCCCCATTAAATGGAGGTCTCCAC 240
Sbjct 914 GATTGGGATACATATCCGTGGTATACATCACAAGGGGTCCCCATTAAATGGAGGTCTCCAC 973
Query 241 AGAACATAAGTTTACAGTACATCTGGAAAAGCTGACCAAGATATTAATTATTACATCC 300
Sbjct 974 AGAACATAAGTTTACAGTACATCTGGAAAAGCTGACCAAGATATTAATTATTACATCC 1033
Query 301 CTGCTGAAGATTTCAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGTGGG 360
Sbjct 1034 CTGCTGAAGATTTCAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGTGGG 1093
Query 361 CCCGGAACCTGGAACCTCAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCGGATA 420
Sbjct 1094 CCCGGAACCTGGAACCTCAAAGATGTTTACAGACAGAAGTCAAGAAAGCTGATTTCGGATA 1153
Query 421 TGGGAAGAAGTGTATCAGCTACCGATATGAAATATTAGCCAAAAGTGACCTTTGAAGAAA 480
Sbjct 1154 TGGGAAGAAGTGTATCAGCTACCGATATGAAATATTAGCCAAAAGTGACCTTTGAAGAAA 1213
Query 481 GTGCAAAAGCTTTTCATGAAGGAAACCATCAAAATGGGAAATTAAGAGCCGACCCAAAGGCC 540
Sbjct 1214 GTGCAAAAGCTTTTCATGAAGGAAACCATCAAAATGGGAAATTAAGAGCCGACCCAAAGGCC 1273

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Query	541	TTTGGGGTATTATTATTATATCTGATTGCCACAATTATAACGTTTATGCCCCAAACTACT	600
Sbjct	1274	TTTGGGGTATTATTATTATATCTGATTGCCACAATTATAACGTTTATGCCCCAAACTA-T	1332
Query	601	-CTGGGTCATGCCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTGGAAC	659
Sbjct	1333	ACTGGGTCATGCCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTGGAAC	1392
Query	660	AGCAGTGCCTGCTTTATATCCTTCTATCGGTGCTCGAAATCCCTTGGAGACAGTGAAAC	719
Sbjct	1393	AGCAGTGCCTGCTTTATATCCTTCTATCGGTGCTCGAAATCCCTTGGAGACAGTGAAAC	1452
Query	720	ATTTTGCCTTCTCCAAATTTCTGGTGTCATGAATCCATGAGGATCTCCACCATGACATCT	779
Sbjct	1453	ATTTTGCCTTCTCCAAATTTCTGGTGTCATGAATCCATGAGGATCTCCACCATGACATCT	1512
Query	780	CATGATTATGCTCTGCCCTGTAATTTGTCTACACAAGGCTAGGGTACAGAGTGAACCTTTA	839
Sbjct	1513	CATGATTATGCTCTGCCCTGTAATTTGTCTACACAAGGCTAGGGTACAGAGTGAACCTTTA	1572
Query	840	TTTTTCCCTTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCTGCCTTGGGAGCT	899
Sbjct	1573	TTTTTCCCTTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCTGCCTTGGGAGCT	1632
Query	900	GCAGGCATTGTTATTTTGGGAGACATGAATTTAACTGCATCCAAGGCCAACTGTACAAG	959
Sbjct	1633	GCAGGCATTGTTATTTTGGGAGACATGAATTTAACTTCATCCAAGGCCAACTGTACAAG	1692
Query	960	GTGAAGCAGTTTGTGAGTTCTGATTTAGGGAGCTACATAGCCAATGTGACCAGAGCTGCT	1019
Sbjct	1693	GTGAAGCAGTTTGTGAGTTCTGATTTAGGGAGCTACATAGCCAATGTGACCAGAGCTGCT	1752
Query	1020	GAGGTATGCAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCATAAGGAAGATGTGGAAC	1079
Sbjct	1753	GAGGTATGCAGCCTTCACCTCTGCAGGAACAACGGGAGGTGCATAAGGAAGATGTGGAAC	1812
Query	1080	GCGCCCAGTTACCTTCACCTTGAACCTGCAAGTTACCACATAGAGGCCTCTGAGGACGGG	1139
Sbjct	1813	GCGCCCAGTTACCTTCACCTTGAACCTGCAAGTTACCACATAGAGGCCTCTGAGGACGGG	1872
Query	1140	GAGTTTACTGTGAAAGGAAAAGCATCTGTATACAGACCTGGCAGTGATGGCAGATACATTT	1199
Sbjct	1873	GAGTTTACTGTGAAAGGAAAAGCATCTGTATACAGACCTGGCAGTGATGGCAGATACATTT	1932
Query	1200	TCCTGTCTATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAATAAAGACGGCTGAT	1259
Sbjct	1933	TCCTGTCTATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAATAAAGACGGCTGAT	1992
Query	1260	GGCTGCTCTGGG	1271
Sbjct	1993	GGCTGCTCTGGG	2004

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>ref|XM_001086758.1| G PREDICTED: Macaca mulatta similar to hyaluronoglucosaminidase 4 (LOC696128), mRNA
Length=1825
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GENE ID: 696128 LOC696128 | similar to hyaluronoglucosaminidase 4  
[Macaca mulatta]

Score = 2154 bits (1166), Expect = 0.0  
Identities = 1238/1273 (97%), Gaps = 4/1273 (0%)  
Strand=Plus/Plus

Query	1	GTCTAAAACCTGCTCGACTTCCAATTTATCAAGAGAAACCTTTTATAGCTGCTTGGAAATG	60
Sbjct	154	GTCTAAAACCTGCTCGACTTCCAATTTATCAAGAGAAACCTTTTATAGCTGCTTGGAAATG	213
Query	61	CTCCAACAGATCAGTGTTTGATAAAATATAATTTAAGACTAAATTTGAAAATGTTTCCTG	120
Sbjct	214	CTCCAACAGATCAGTGTTTGATAAAATATAATTTAAGACTAAATTTGAAAATGTTTCCTG	273
Query	121	TGATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAAATGCTACTATATTTTATGTCAACA	180



Sbjct	274	TGATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAATGTCACTATATTTTATGTCAACA	333
Query	181	GATTGGGATACACTCCGTGGTATACATCACAAGGGGTCGCCATTAATGGAGGTCTCCAC	240
Sbjct	334	GATTGGGATACATTCATCGGTATACATCACAAGGGGTCGCCATTAATGGAGGTCTCCAC	393
Query	241	AGAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACATCC	300
Sbjct	394	AGAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACATCC	453
Query	301	CTGCTGAAGATTTCAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCAAGTGGG	360
Sbjct	454	CTGATGAAGATTTCAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCAAGTGGG	513
Query	361	CCCGGAACTGGAAC - CAAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCGAT	419
Sbjct	514	CCCGGAACTGGAAC - TGCAAAAGACGCTACAGAAAGAAGTCAAGAAAGCTTATTAACGAT	572
Query	420	ATGGGAAAGAAATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAGAA	479
Sbjct	573	ATGGGAAAGAAATGTATCAGCTACCGATATTGAATATTTAGCTAAAGTGACCTTTGAAGAA	632
Query	480	AGTGCAAAAGCTTTCATGAAGGAAACCATCAAAATGGGAATTAAAGAGCGACCCAAAGGC	539
Sbjct	633	AGCGCAAAAGCTTTCATGAAGGAAACCATCAAAATGGGAATTAAAGAGTCGACCCAAAGGT	692
Query	540	CTTTGGGGTTATTATTATATCCTGATTGCCCAATTAACAGTTTATGCCCAAAGTAC	599
Sbjct	693	CTTTGGGGTTATTATTATATCCTGATTGTCACAATTAATAGTTTATGCCCAAACATA-	751
Query	600	T-CTGGGTCATGCCCAGAAGACGAAGTCTTGAGGAACAAATGAGCTCTCTGGCTCTGGAA	658
Sbjct	752	TACTGGGTCATGCCCAGAAGAGGAAGTCTTGAGGAACAAATGAGCTCTCTGGCTCTGGAA	811
Query	659	CAGCAGTGCTGCTTTATATCCTTCTATCGGTGTCTGGAATCCCTTGGAGACAGTGAAAA	718
Sbjct	812	CAGCAGTGCTGCTTTATATCCTTCTATCGGTGTCTGGAATCCCTTGGAGACAGTGAAAA	871
Query	719	CATTTTGCCTTCTCCAAATTTTCGGGTGCATGAATCCATGAGGATCTCCACCATGACATC	778
Sbjct	872	CATTTTGCCTTCTCCCAATTTTCGGGTACATGAATCCATGAGGATCTCCACCATGACATC	931
Query	779	TCATGATTATGCTCTGCCTGTATTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTT	838
Sbjct	932	TCATGATTATGCTCTGCCTGTATTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTT	991
Query	839	ATTTTTCCTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCTGCCTTGGGAGC	898
Sbjct	992	ATTTTTCCTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCTGCCTTGGGAGC	1051
Query	899	TGCAGGCATTGTTATTTTGGGGAGACATGAATTTAACTGCATCCAAGGCCAAGTACAAA	958
Sbjct	1052	TGCAGGCATTGTTATTTTGGGGAGACATGAATTTAACTTCATCCAAGGCCAAGTACAAA	1111
Query	959	GGTGAAGCAGTTTGTGAGTTCGTATTAGGGAGCTACATAGCCAAATGTGACCAGAGCTGC	1018
Sbjct	1112	GGTGAAGCAGTTTGTGAGTTCGTATTAGGGAGCTACATAGCCAAATGTGACCAGAGCTGC	1171
Query	1019	TGAGGTATGCAGCCTTCACTCTGCAGGAACAATGGCAGGTGCATTAAGGAAGATGTGGAA	1078
Sbjct	1172	TGAGGTATGCAGCCTTCACTCTGCAGGAACAATGGGAGGTGCATTAAGGAAGATGTGGAA	1231
Query	1079	CGCGCCAGTTACCTTCACTTGAACCCCTGCAAGTTACCATAGAGGCCCTCTGAGGACGG	1138
Sbjct	1232	CTCACCCTTACCTTCACTTGAACCCCGAAGTTACCATAGAGGCCCTCTGAGGATGG	1291
Query	1139	GGAGTTTACTGTGAAAGGAAAAGCATCTGATACAGACCTGGCAGTGATGGCAGATACATT	1198
Sbjct	1292	AGAAATTTACTGTGAAAGGAAAGCATCTGATACAGACCTGGCAGTGATGGCAGATACATT	1351
Query	1199	TTCTGTCAATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAATAAAGACGGCTGA	1258
Sbjct	1352	TTCTGTCAATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAATAAAGACGGCTGA	1411
Query	1259	TGGCTGCTCTGGG 1271	

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Sbjct 1412 TGGCTGTTCTGGG 1424

>ref|XM\_001502389.1| **G** PREDICTED: Equus caballus similar to Hyaluronoglucosaminidase 4 (LOC100056514), mRNA  
Length=1553

**GENE ID: 100056514 LOC100056514** | similar to Hyaluronoglucosaminidase 4 [Equus caballus]

Score = 1742 bits (943), Expect = 0.0

Identities = 1165/1274 (91%), Gaps = 8/1274 (0%)

Strand=Plus/Plus

Query	2	TCTAAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGGAAATGC	61
Sbjct	173	TCTAAAACCTGCCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCATGGAATGC	232
Query	62	TCCACAGATCAGTGTTTGATAAAATATAATTTAAGACTAAATTTGAAAATGTTTCTGT	121
Sbjct	233	TCCACAGATCAGTGTTTGATAAAATATAATATAAGACTAAATCTGAAAATGTTTTCAGGT	292
Query	122	GATTGGAAGCCCACTGGCCAAGGCCAGGGGCAAAATGTCACTATATTTATGTCAACAG	181
Sbjct	293	GATTGGAAGCCCACTGGCCAAGGCTAGAGGGCAAAATGTCACTATATTTATGTCAACAG	352
Query	182	ATTGGGATACTATCCGTGGTATACATCAAGGGGTCCCCATTATGGAGGTCTCCACACA	241
Sbjct	353	ATTGGGCTACTATCCATGGTATACATCAAGGGGTTCCTGTTAACGGGGTCTCCCCCA	412
Query	242	GAACATAAGTTTACAAGTACATCTGAAAAAGCTGACCAAGATATTAAATTATTACATCCC	301
Sbjct	413	GAACATAAGTTTGAAGTACACTAGAAAAAGCTGACGAAGATATTAAATTACTACATCCC	472
Query	302	TGCTGAAGATTTCAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGTGGGC	361
Sbjct	473	TGCTGAAGATTTCAGTGGACTTGCTGTCTAGACTGGGAATATTGGAGACCCAGTGGGC	532
Query	362	CCGGAAGCTGGAACTCAAAGATGTTACAGACAGAAGTCAAGAAAGCTTATTTCCGATAT	421
Sbjct	533	CCGGAAGCTGGAACTCAAAGATGTTACAGACAGAAGTCAAGAAAGCTTATTTCTGATAT	592
Query	422	GGGAA-AGAATGTATCAGCTACCGATATTGAATATTAGCCAAAGTGACCTTTGAAGAAA	480
Sbjct	593	GC-AAGAGAATGTATCAGCTACTGATATTGAATATTAGCTAAAGCAACCTTTGAAGAAA	651
Query	481	GTGCAAAAGCTTTTCATGAAGGAAACCATCAAATTTGGGAATTAAGAGCCGACCCAAAGGCC	540
Sbjct	652	GTGCAAAAGCTTTTATGAAGGAAACCATCGAATTTGGGAATTAAGAGCCGACCCAAAGGCC	711
Query	541	TTTGGGGTTATTATTTATATCTGATTGCCACAAATTATAACGTTTATGCCCCAAACTACT	600
Sbjct	712	TTTGGGGTTATTATTTATATCTGATTGCCACAAATTATAATGTTTATGACCCAAACTA-T	770
Query	601	-CTGGGTCATGCCAGAACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTGGAAC	659
Sbjct	771	ACTGGGTCATGCCAGAACGAAGTCTTGAGAAATAATGAGCTCTCTTGGCTCTGGAAC	830
Query	660	AGCAGTGTGCTTTATATCCTTCTATCGGTGTCTGGAATCCCTTGGAGACAGTGAAAC	719
Sbjct	831	AGCAGTGTGCTTTATATCCTTCTATGGTGTCTGGAATCTCTTGGAGACAGCGAAAC	890
Query	720	ATTTTGCCTTCTC-CAAAATTCGGGTGTCATGAATCCATGAGGATCTCCACCATGACATC	778
Sbjct	891	ATTTTGCCTTCTCGCAA-TTTCGGGTGTCATGAATCCATGAGGATCTCCACCATGACATC	949
Query	779	TCATGATTATGCTCTGCGGTGATTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTT	838
Sbjct	950	CCACGATTATGCTCTGCGGTGATTGTCTACACAAGACTAGGCTACAGAGACGAACCTTT	1009
Query	839	ATTTTTCCTTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGTCTGCTTGGGAGC	898
Sbjct	1010	ATTTTTCCTTTCTAAGCAAGATCTAATCAGTACCATTGGAGAAAGCGCTGCTTGGGAGC	1069
Query	899	TGCAGGCATTGTTATTTCGGGGAGACATGAATTTAACTGCATCCAAGGCCAAGCTGTACAAA	958

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Sbjct 1070 TGCAGGCTTTGTTATTTGGGGAGACATGAATTTAACTTCATCTGAGGGCAACTGTACAAA 1129
Query 959 GGTGAAGCAGTTTGTGAGTCTGATTTAGGGAGCTACATAGCCAAATGTGACCAGAGCTGC 1018
Sbjct 1130 GGTGAAGCAGTTTGTGAGCTCTGTTTATAGGGCGCTACATAGTCAACGTGACCCGAGCGCG 1189
Query 1019 TGAGGTATGCAGCCTTCACCTCTGCAGGAACAATGGCAGTGTCATAAGGAAGATGTGGAA 1078
Sbjct 1190 CGAGGCGTGCAGCCTCCACCTGTGCAGGAACAACGGGAGATGCCGTGAGGAAGGTGTGGAA 1249
Query 1079 CGCGCCC-AGTTACCTTCACCTGAACCCCTGCAAGTTACCACATAGAGGCCCTCTGAGGACG 1137
Sbjct 1250 AGCTCCCGA-TTACCTTCATTGAACCCCTGCAAGTTACTACATAGAGGCCCTCCGAGGATG 1308
Query 1138 GGGAGTTTACTGTGAAAGGAAAAGCATCTGATACAGACCTGGCAGTGATGGCAGATACAT 1197
Sbjct 1309 GAGAAATTTATGTGGAAGGAAAAGCATCTGATACAGACCTGGCCCTGATGGCAGAGAAAT 1368
Query 1198 TTTCCCTGTCTATTGTTATCAGGGATATGAAGGAGCTGATTGCGAGAGAAATAAGACGGCTG 1257
Sbjct 1369 TTTCCCTGTCTAGTGTATTACAGGGATACGAAGGGGCGATTGCGAGAGAAATGAAGACAGCTG 1428
Query 1258 ATGGCTGCTCTGGG 1271
Sbjct 1429 ATGGCTGCTCTGGG 1442

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>ref|XM\_532444.2| **UEG** PREDICTED: Canis familiaris similar to hyaluronoglucosaminidase 4, transcript variant 1 (LOC475212), mRNA  
Length=1761

GENE ID: 475212 HYAL4 | hyaluronoglucosaminidase 4 [Canis lupus familiaris]

Score = 1659 bits (898), Expect = 0.0  
Identities = 1154/1278 (90%), Gaps = 16/1278 (1%)  
Strand=Plus/Plus

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Query 2 TCTAAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGGAAATGC 61
Sbjct 102 TCTAAAACCTGCCCGGCTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGGAAATGC 161
Query 62 TCCAACAGATCAGTGTTTGATAAAAATATAATTTAAGACTAAATTTGAAAATGTTTCTGT 121
Sbjct 162 CCCAACGGATCAGTGTTTGATAAAAATACAATATAGGATTAAATTTGAAAATGTTTTCAGGT 221
Query 122 GATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAAATGTCACATATATTTATGTCAACAG 181
Sbjct 222 TATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAAATATCACTATATTTATGTCAACAG 281
Query 182 ATTGGGATACTATCCGTGGTATACATCACAAGGGGTCCCATTAATGGAGGTCTCCCA 241
Sbjct 282 ATTGGGATACTATCCATGGTATACATCACAGGGGGTTCCTTAATGGGGGTCTCCCA 341
Query 242 GAACATAAGTTTACAAGTACATCTGAAAAAGCTGACCAAGATATTAATTTATACATCCC 301
Sbjct 342 GAACATAAGTTTGAAGTGCATCTAGAAAAAGCTGACCAAGATATTAATTTATACATCCC 401
Query 302 TGCTGAAGATTTCAAGTGGACTTGCTGTTATAGATTGGGAAATATTGGCGACCACAGTGGGC 361
Sbjct 402 TGCTGAAGATTTCAATGGACTGGCTGTTATAGACTGGGAATACTGGCGACCTCAAGTGGGC 461
Query 362 CCGGAACCTGGAACCTCAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCGATAT 421
Sbjct 462 CCGTAACCTGGAACCAAAAAGATGCTCTACAGACAGAAGTCAAGAAAGCTGATTTCTGACAT 521
Query 422 GGGAA-AGAATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAGAAA 480
Sbjct 522 GC-AAGAGAAATGATCAGCTACTGATATTGAATATTTAGCCAAAGCAACCTTTGAAGAAA 580
Query 481 GTGCAAAAGCTTTTCATGAAGGAAACCATCAAATGGGAAATTAAGAGCCGACCAGAAAGG-C 539
Sbjct 581 GTGCAAAAGCTTTTCATGAAGGAAACCATCGAATTTGGGAATTAAGAGTAGACC-AAAGGGC 639
Query 540 CTTTGGGGTTATTATTTATATCTGTGTCACAATATATAAGTTTATGCCCCAACTAC 599

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Sbjct 640      CTC TGGGGT TATTATTTATATCTGATTGCCACAATTTATAATGTTTATGCCCCAAATTA- 698
Query 600      T-CTGGGTCATGCCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTGGAA 658
Sbjct 699      TACTGGGTCATGCCCAGAAGAGGAAGTTTGAGAAACAATGAGCTCTCTTGGCTCTGGAA 758
Query 659      CAGCAGTGCCTGCTTTATATCCTTCTATCGGTGCTCTGGAAATCCCTTGAGACAGTGA AAA 718
Sbjct 759      TAGTAGTGTCTGCTTTATATCCTTCTATTTGGTGTGAGAAAATCTCTTGAAGACAATGA AAA 818
Query 719      CATTTTGCCTCTCTC-CAAAATTCGGGTGCATGAATCCATGAGGATCTCCACCATGACAT 777
Sbjct 819      CATTTTGCCTCTCTCGGA-TTTCGAGTGCATGAATCCCTGAGGATCTCCACCATGACAT 877
Query 778      CTCATGATTATGCTCTGCCTGTATTTGTCTACACAAGGCTAGGGTACAGAGATGAACCTT 837
Sbjct 878      CCCATGATTATGCTCTGCCTATATTTGTCTACACAAGGCTAGGCTACAGAAATGAGCCCT 937
Query 838      TATTTTTCTTTCTTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGTGCTTGGGAG 897
Sbjct 938      TATTTTTCTTTCTTAAGCAAGATCTAATCAGTACTATTGGAGAAAGTGTGCTTGGGAG 997
Query 898      CTGCAGGCATGTGTTATTTGGGGAGACATGAATTTAACTGCATCCAGGGCCAAGTGTACAA 957
Sbjct 998      CTGCAGGCATGTGTTATCTGGGGAGACATGAATTTAACTTCATCTGAGGGCAACTGTACAA 1057
Query 958      AGGTGAAGCAGTTTGTGAGTTCTGATTTAGGG-AGTCACATAGCCAATGTGACCAGAGCT 1016
Sbjct 1058      AGGTGAAGCAGTATGTGAGTTCTGACTTAGGACA-CTACATAGTCAATGTGACCAGAGCG 1116
Query 1017      GCTGAGGTATGCAGCCTTACCTCTGCAGGAACAATGCGAGGTGCATAAGGAAGATGTGG 1076
Sbjct 1117      GCTGAGGTGTGCAGCCTTACCTGTGCAGGAGTAATGGGAGATGCATAAGGAAGGTATGG 1176
Query 1077      AACGCGCCC-AGTTACCTTCACTTGAACCTTGCAAGTTACCACATAGAGGCCTCTGAGGA 1135
Sbjct 1177      AAAGCTCTCGA-TTACCTGCACTTGAACCTTGCAAGTTACCACATAGAGGCCTCCAAGGA 1235
Query 1136      CGGGGAGTTTACTGTGAAAGGAAAAGCATCTGATACAGACCTGGCAGTGTGGCAG-ATA 1194
Sbjct 1236      TGGAGAATTTATTTGTGAAAGGAAAAGCATCTGATATGGAACCTGGAAGCGCTTGG-AGGAGA 1294
Query 1195      CA-TTTTCTCTGTCATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAATAAAGACG 1253
Sbjct 1295      -AGTTTCTCTGTCAGTGTATCAGGGATACGAAGGAGCCGACTGTAGAGGAACAAAGACG 1353
Query 1254      GCTGATGGCTGCTCTGGG 1271
Sbjct 1354      GCTGACGGCTGCTCTGGG 1371

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>gb|AC006029.2|  Homo sapiens BAC clone GS1-195F7 from 7q31.2-q32, complete seq  
Length=143851

Sort alignments for this  
E value Score Perce  
Query start position

Score = 1578 bits (854), Expect = 0.0  
Identities = 854/854 (100%), Gaps = 0/854 (0%)  
Strand=Plus/Plus

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Query 1      GTCTAAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGAATG 60
Sbjct 115835  GTCTAAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGAATG 1158
Query 61      CTCCAACAGATCAGTGTGATAAAATATAATTTAAGACTAAATTTGAAAATGTTTCCTG 120
Sbjct 115895  CTCCAACAGATCAGTGTGATAAAATATAATTTAAGACTAAATTTGAAAATGTTTCCTG 1159
Query 121     TGATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAATGTCACTATATTTTATGTCACAA 180
Sbjct 115955  TGATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAATGTCACTATATTTTATGTCACAA 1160

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Query	181	GATTGGGATACTATCCGTGGTATACATCAAAAGGGGTCCCCATTAATGGAGGTCTCCAC	240
Sbjct	116015	GATTGGGATACTATCCGTGGTATACATCAAAAGGGGTCCCCATTAATGGAGGTCTCCAC	1160
Query	241	AGAACATAAGTTTACAAGTACATCTGAAAAAGCTGACCAAGATATTAATTATTACATCC	300
Sbjct	116075	AGAACATAAGTTTACAAGTACATCTGAAAAAGCTGACCAAGATATTAATTATTACATCC	1161
Query	301	CTGCTGAAGATTTCAGTGGACTTGCCTGTTATAGATTGGGAATATTGGCGACCACAGTGGG	360
Sbjct	116135	CTGCTGAAGATTTCAGTGGACTTGCCTGTTATAGATTGGGAATATTGGCGACCACAGTGGG	1161
Query	361	CCCGGAACCTGGAACCTCAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCGATA	420
Sbjct	116195	CCCGGAACCTGGAACCTCAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCGATA	1162
Query	421	TGGGAAAGAAATGTATCAGCTACCGATATTGAATATTATGCCAAAGTGACCTTTGAAGAAA	480
Sbjct	116255	TGGGAAAGAAATGTATCAGCTACCGATATTGAATATTATGCCAAAGTGACCTTTGAAGAAA	1163
Query	481	GTGCAAAAAGCTTTCATGAAGGAAACCATCAAATTTGGGAATTAAGAGCCGACCCAAAGGCC	540
Sbjct	116315	GTGCAAAAAGCTTTCATGAAGGAAACCATCAAATTTGGGAATTAAGAGCCGACCCAAAGGCC	1163
Query	541	TTTGGGGTTATTATTATATCTGATTCGCACAATTATAACGTTTATGCCCCAACTACT	600
Sbjct	116375	TTTGGGGTTATTATTATATCTGATTCGCACAATTATAACGTTTATGCCCCAACTACT	1164
Query	601	CTGGGTCATGCCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTGGAACA	660
Sbjct	116435	CTGGGTCATGCCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTGGAACA	1164
Query	661	GCAGTGTCTGCTTTATATCCTTCTATCGGTGCTCGGAAATCCCTTGGAGACAGTGAATAACA	720
Sbjct	116495	GCAGTGTCTGCTTTATATCCTTCTATCGGTGCTCGGAAATCCCTTGGAGACAGTGAATAACA	1165
Query	721	TTTTGCGCTTCTCCAAATTTTCGGGTGCATGAATCCATGAGGATCTCCACCATGACATCTC	780
Sbjct	116555	TTTTGCGCTTCTCCAAATTTTCGGGTGCATGAATCCATGAGGATCTCCACCATGACATCTC	1166
Query	781	ATGATTATGCTCTGCCTGTATTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTTAT	840
Sbjct	116615	ATGATTATGCTCTGCCTGTATTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTTAT	1166
Query	841	TTTTCCTTTCTAAG	854
Sbjct	116675	TTTTCCTTTCTAAG	116688

Score = 608 bits (329), Expect = 2e-170  
 Identities = 329/329 (100%), Gaps = 0/329 (0%)  
 Strand=Plus/Plus

Query	943	AGGCCAACTGTACAAAGGTGAAGCAGTTTGTGAGTTCTGATTTAGGGAGCTACATAGCCA	1002
Sbjct	124213	AGGCCAACTGTACAAAGGTGAAGCAGTTTGTGAGTTCTGATTTAGGGAGCTACATAGCCA	1242
Query	1003	ATGTGACCAGAGCTGCTGAGGTATGCAGCCTTCACTCTGCAGGAACAATGGCAGGTGCA	1062
Sbjct	124273	ATGTGACCAGAGCTGCTGAGGTATGCAGCCTTCACTCTGCAGGAACAATGGCAGGTGCA	1243
Query	1063	TAAGGAAGATGTGGAACGCGCCAGTTACCTTCACTTGAACCTTGAAGTTACACATAG	1122
Sbjct	124333	TAAGGAAGATGTGGAACGCGCCAGTTACCTTCACTTGAACCTTGAAGTTACACATAG	1243
Query	1123	AGGCCTCTGAGGACGGGAGTTTACTGTGAAAGGAAAAGCATCTGTATACAGACCTGGCAG	1182
Sbjct	124393	AGGCCTCTGAGGACGGGAGTTTACTGTGAAAGGAAAAGCATCTGTATACAGACCTGGCAG	1244
Query	1183	TGATGGCAGATACATTTTCTCTGTCATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAG	1242
Sbjct	124453	TGATGGCAGATACATTTTCTCTGTCATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAG	1245
Query	1243	AAATAAAGACGGCTGATGGCTGCTCTGGG	1271
Sbjct	124513	AAATAAAGACGGCTGATGGCTGCTCTGGG	124541

Score = 172 bits (93), Expect = 3e-39  
 Identities = 96/97 (98%), Gaps = 1/97 (1%)  
 Strand=Plus/Plus

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Query 849      TCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTCTGCCTTGGGAGCTGCAGGCATT 908
Sbjct 122217   TCT-AGCAAGATCTAGTCAGCACCATAGGAGAAAGTCTGCCTTGGGAGCTGCAGGCATT 1222

Query 909      GTTATTGGGGAGACATGAATTTAACTGCATCCAAGG 945
Sbjct 122276   GTTATTGGGGAGACATGAATTTAACTGCATCCAAGG 122312
  
```

>gb|AC197510.3| **D** Pan troglodytes BAC clone CH251-712N23 from chromosome 7, comp  
 sequence  
 Length=179287

Sort alignments for this  
 E value Score Perce  
 Query start position

Score = 1539 bits (833), Expect = 0.0  
 Identities = 848/855 (99%), Gaps = 2/855 (0%)  
 Strand=Plus/Minus

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Query 1      GTCTAAACCTGCTCGACTTCCAATTTTCAAAGGAAACCTTTTATAGCTGCTTGGAAATG 60
Sbjct 87065   GTCTAAACCTGCTCGACTTCCAATTTTCAAAGGAAACCTTTTATAGCTGCTTGGAAATG 87006

Query 61      CTCCAACAGATCAGTGTTTGATAAAATATAATTTAAGACTAAATTTGAAAATGTTTCCTG 120
Sbjct 87005   CTCCAACAGATCAGTGTTTGATAAAATATAATTTAAGACTAAATTTGAAAATGTTTCCTG 86946

Query 121     TGATTGGAAGCCCACTGGCCAGGCCAGGGGGCAAAATGTCACATATATTTTATGTCAACA 180
Sbjct 86945   TGATTGGAAGCCCACTGGCCAGGCCAGGGGGCAACATGTCACATATATTTTATGTCAACA 86886

Query 181     GATTGGGATACTATCCGTGGTATACATCACAAGGGGTCCCCATTAAATGGAGGTCTCCAC 240
Sbjct 86885   GATTGGGATACTATCCGTGGTATACATCACAAGGGGTCCCCATTAAATGGAGGTCTCCAC 86826

Query 241     AGAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACATCC 300
Sbjct 86825   AGAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACATCC 86766

Query 301     CTGCTGAAGATTTTCAGTGGACTTGCTGTTTATAGATTGGGAATATTGGCGACCAAGTGGG 360
Sbjct 86765   CTGCTGAAGATTTTCAGTGGACTTGCTGTTTATAGATTGGGAATATTGGCGACCAAGTGGG 86706

Query 361     CCCGGAACCTGGAACTCAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCGATA 420
Sbjct 86705   CCCGGAACCTGGAACTCAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCGATA 86646

Query 421     TGGGAAAGAAATGATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAGAAA 480
Sbjct 86645   TGGGAAAGAAATGATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAGAAA 86586

Query 481     GTGCAAAAGCTTTTCATGAAGGAAACCATCAAATGGGAATTAAGAGCCGACCCAAAGGCC 540
Sbjct 86585   GTGCAAAAGCTTTTCATGAAGGAAACCATCAAATGGGAATTAAGAGCCGACCCAAAGGCC 86526

Query 541     TTTGGGGTTATTATTATATCTGATTGCCACAATTATAACGTTTATGCCCCAAACTACT 600
Sbjct 86525   TTTGGGGTTATTATTATATCTGATTGCCACAATTATAACGTTTATGCCCCAAACTA-T 86467

Query 601     -CTGGGTCTATGCCAGAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTGGAAC 659
Sbjct 86466   ACTGGGTCTATGCCAGAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTGGAAC 86407

Query 660     AGCAGTGTCTGCTTTATATCCTTCTATCGGTGTCTGGAATCCCTTGGAGACAGTGAAAAC 719
Sbjct 86406   AGCAGTGTCTGCTTTATATCCTTCTATCGGTGTCTGGAATCCCTTGGAGACAGTGAAAAC 86347
  
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Query 720      ATTTTGCAGCTTCTCCAAATTTTCGGGTGCATGAATCCATGAGGATCTCCACCATGACATCT 779
Sbjct 86346    ATTTTGCAGCTTCTCCAAATTTTCGGTGTGCATGAATCCATGAGGATCTCCACCATGACATCT 86287

Query 780      CATGATTATGCTCTGCCTGTATTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTTTA 839
Sbjct 86286    CATGATTATGCTCTGCCTGTATTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTTTA 86227

Query 840      TTTTTCCTTTCTTAAG 854
Sbjct 86226    TTTTTCCTTTCTTAAG 86212

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Score = 592 bits (320), Expect = 2e-165  
 Identities = 326/329 (99%), Gaps = 0/329 (0%)  
 Strand=Plus/Minus

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Query 943      AGGCCAACTGTACAAAGGTGAAGCAGTTTGTGAGTTCTGATTTAGGGAGCTACATAGCCA 1002
Sbjct 78688    AGGCCAACTGTACAAAGGTGAAGCAGTTTGTGAGTTCTGATTTAGGGAGCTACATAGCCA 78629

Query 1003     ATGTGACCAGAGCTGCTGAGGTATGCAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCA 1062
Sbjct 78628    ATGTGACCAGAGCTGCTGAGGTATGCAGCCTTCACCTCTGCAGGAACAACGGGAGGTGCA 78569

Query 1063     TAAGGAAGATGTGGAACGCCCCAGTTACCTTCACTTGAACCCCTGCAAGTTACCACATAG 1122
Sbjct 78568    TAAGGAAGATGTGGAACGCCCCAGTTACCTTCACTTGAACCCCGCAAGTTACCACATAG 78509

Query 1123     AGGCCTCTGAGGACGGGGAGTTTACTGTGAAAGGAAAAGCATCTGATACAGACCTGGCAG 1182
Sbjct 78508    AGGCCTCTGAGGACGGGGAGTTTACTGTGAAAGGAAAAGCATCTGATACAGACCTGGCAG 78449

Query 1183     TGATGGCAGATACATTTTCTGTCTATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAG 1242
Sbjct 78448    TGATGGCAGATACATTTTCTGTCTATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAG 78389

Query 1243     AAATAAAGACGGCTGATGGCTGCTCTGGG 1271
Sbjct 78388    AAATAAAGACGGCTGATGGCTGCTCTGGG 78360

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Score = 167 bits (90), Expect = 1e-37  
 Identities = 95/97 (97%), Gaps = 1/97 (1%)  
 Strand=Plus/Minus

```

Query 849      TCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGTGCCTTGGGAGCTGCAGGCATT 908
Sbjct 80678    TCT-AGCAAGATCTAGTCAGCACCATAGGAGAAAGTGTGCCTTGGGAGCTGCAGGCATT 80620

Query 909      GTTATTTGGGGAGACATGAATTTAACTGCATCCAAGG 945
Sbjct 80619    GTTATTTGGGGAGACATGAATTTAACTTCATCCAAGG 80583

```

>gb|BC132096.1| **UG** Mus musculus hyaluronoglucosaminidase 4, mRNA (cDNA clone MG IMAGE:40130373), complete cds  
 Length=2088

GENE ID: 77042 **Hyal4** | hyaluronoglucosaminidase 4 [Mus musculus]  
 (Over 10 PubMed links)

Score = 1339 bits (725), Expect = 0.0  
 Identities = 1089/1262 (86%), Gaps = 36/1262 (2%)  
 Strand=Plus/Plus

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Query 3        CTAAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGGAAATGCT 62
Sbjct 320      CTAAAACCTGCCCGACTTCCAGTTTATCAAAGGAAACCTTTTATGCTGCTTGGAAATGCT 379

Query 63       CCAACAGATCAGTGTTTTGATAAAATATAATTTAAGACTAAATTTGAAAA-TGTTTCCTG- 120
Sbjct 380      CCAACAGACCTGTGTTTGATAAAATATAATTTAAGACTGAACTT-AAAAGTGTTT-CAGA 437

Query 121      TGATTGGAAGCCCACTGGC-CAAGGCCAGGGGGCAAATGTCACTATATTTTATGTCAAC 179

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Sbjct	438	TGGTTGGAAGCCCTC - GGCTCAAAGACAGGGGGCAAATGTGTTATATTTTATGCCAAC	496
Query	180	AGATTGGGATACTATCCGTGGTATACATCACAAAGGGTCCCCATTAATGGAGGTC - TCCC	238
Sbjct	497	AGATTGGGATATTACCCATGGTATACATCAGAAGGGGTACCCATCAATGGTGGCTCTCCC	556
Query	239	ACAGAACATAAGTTTACAAGTACACTCGGAAAAAGCTGACCAAGATATTAATTATACAT	298
Sbjct	557	-CAAAACACAAAGCTTACAAGTACACCTGAAAAAGCTGCCCAGGATATTAATTATACAT	615
Query	299	CCCTGCTGAAGATTTTCAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGTG	358
Sbjct	616	CCCTTCTGAAAAATTTTCAGTGGACTTGCTGTTATAGACTGGGAATATTGGCGCCACAGTG	675
Query	359	GGCCCGGAAC TGGAAC TCAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTTCGA	418
Sbjct	676	GGCCCGGAAC TGGAACA CAAAGGATATCTACAGACAGAAGTCAAGAACTCTTATTTCTGA	735
Query	419	TATGGGAA - AGAATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAG	477
Sbjct	736	TAT - GAAAGAGAACATATCTGCTGCTGATATTGAATATTCAGCCAAAGCAACTTTTG - AG	793
Query	478	-AAAGTGCAAAAGCTTTTCATGAAGGAAACCATCAAATTTGGGAATTAAGAGCCGACCCAAA	536
Sbjct	794	AAAAGTGCAAAAGCTTTTCATGGAGGAAACTATCAAATTTGGGAAGTAAGAGCAGACCCAAAG	853
Query	537	GGCCTTTGGGGTTATTATTATATCTGATTGCCCACAAATATAAGCTTTATGCCCCAAAC	596
Sbjct	854	GGCCTTTGGGGTTATTATTATATCTGATTGCCCACAAATATAATGTTTATGCCCAAAAC	913
Query	597	TACT - CTGGGTCATGCCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGCTCTG	655
Sbjct	914	TA - TACTGGGTCATGCCCAGAAGAGGAAGTTTGAGGAACAATGACCTCTCTTGCTCTG	972
Query	656	GAACAGCAGTGCTGCTTTATATCCTTCTATCGGTGCT - GGAATCCCTTGGAGACAGTG	714
Sbjct	973	GAACAGCAGTACAGCCCTGTATCCTGCTGTCAGTAT - TAGGAAATCCTTTGCAGACAGTG	1031
Query	715	AAAACATTTTTCGCTTCTC - CAAATTTTCGGGTGCATGAATC - CATGAGGATCTCCACCAT	772
Sbjct	1032	AAAACACTTTGCACTTCTCACGA - TTTTCGGGTGCGTGAATCAC - TGAGGATTTCCACCAT	1089
Query	773	GACATCTCATGATTATGCTCTGCCTGATTTGTCTACACA - AGGCTAGGG - TACAGAGAT	830
Sbjct	1090	GACATCACAGGATTATGCTCTGCCTGATTTGTCTACACAG - CT - GGGCTACAAAGAG	1147
Query	831	GAACCTTTATTTTTCCTTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGTCTGCC	890
Sbjct	1148	GAACCTTTACTTTTTCCTTTCTAAGCAAGATCTAATTAGTACCATAGGAGAAAGTGTCTGCC	1207
Query	891	TTGGGAGCTGCAGGCATTGTTATTTGGGGAGACATGAATTTAACTGCATCCAAGGCCAAC	950
Sbjct	1208	TTGGGAGCGCAGGCATTGTTGTTTGGGGAGACATGAATTTAACTTCATCTGAGGAGAAC	1267
Query	951	TGTAC - AAAGGTGAAGCAG - TTGTGTAGTTCTGATTTAGGGAGCTACATAGCCCAATGTGA	1008
Sbjct	1268	TGTACGAAG - TGAACC - GCTTTGTGAATCTGATTTTGGCAGCTACATAATCAATGTGA	1325
Query	1009	CCAGAGCTGCTGAGGTATGCAGCCTTACCTCTGCAGGAACAATGGCAGGTGCATAAGGA	1068
Sbjct	1326	CCAGAGCAGCTGAGGTGTGCACTGCTCACCTTTGCAAGAATAATGGGAGGTGTGTACGGA	1385
Query	1069	AGATGTGGAACGC - GCCCAGTTACCTTCACTTGAACCCCTGCAAGTTACACATAGAGGCC	1127
Sbjct	1386	AGACATGGAAGCAGCTCA - TTACCTCCATTGAACCCCTGCAAGTTACACATAGAGGCC	1444
Query	1128	TCTGAGGACGGGGAGTTTACT - GTGAAAGGAAAAGCATCTGATACAGACCTGGCAGTGAT	1186
Sbjct	1445	TCTGAGGATGGAGAATTCA - TAGTGAGGGGAAGAGCATCAGACACTGACCTAGCTGTGAT	1503
Query	1187	GGCAGATACATTTTCTC - -GTCATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAA	1244
Sbjct	1504	GGCAGAGA - ATTT - CCTATGTCACCTGTTATGAGGGATATGAGGGGCTGACTGTAGAGAA	1561
Query	1245	AT 1246	



Sbjct 1562 AT 1563

>ref|NM\_029848.1| **UEG** Mus musculus hyaluronoglucosaminidase 4 (Hyal4), mRNA  
 gb|BC125402.1| **UG** Mus musculus hyaluronoglucosaminidase 4, mRNA (cDNA clone MG  
 IMAGE:40129917), complete cds  
 Length=2088

GENE ID: 77042 Hyal4 | hyaluronoglucosaminidase 4 [Mus musculus]  
 (Over 10 PubMed links)

Score = 1339 bits (725), Expect = 0.0  
 Identities = 1089/1262 (86%), Gaps = 36/1262 (2%)  
 Strand=Plus/Plus

Query	3	CTAAAACTGCTCGACTTCCAAATTTATCAAAGGAAACCTTTTATAGCTGCTTGGAAATGCT	62
Sbjct	320	CTAAAACTGCCGACCTCCAGTTTATCAAAGGAAACCTTTTATTGCTGCTTGGAAATGCT	379
Query	63	CCAACAGATCAGTGTTTGATAAAATATAATTTAAGACTAAATTTGAAAA-TGTTTCCTG-	120
Sbjct	380	CCAACAGACCTGTGTTTGATAAAATATAATTTAACACTGAACCT-AAAAGTGTTT-CAGA	437
Query	121	TGATTGGAAGCCCACTGGC-CAAGGCCAGGGGGCAAATGTCACTATATTTTATGTCAAC	179
Sbjct	438	TGGTTGAAGCCCTC-GGCTCAAAGACAGGGGGCAAATGTGTTTATATTTATGCCAAC	496
Query	180	AGATTGGGATACTATCCGTGGTATACATCACAAGGGGTCCCCATTATGGAGGTC-TCCC	238
Sbjct	497	AGATTGGGATATTACCATGGTATACATCAGAAGGGGTACCATCAATGTGTGCTTCCCC	556
Query	239	ACAGAACATAGTTTACAAGTACATCTGGAAGGCTGACCAAGATATTAAATATTACAT	298
Sbjct	557	-CAAAACACAAGCTTACAAGTACACCTGAAAAAGCTGCCCAGGATATTAAATATTACAT	615
Query	299	CCCTGCTGAAGATTTCACTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGTG	358
Sbjct	616	CCCTTCTGAAAAATTTCACTGGACTTGCTGTTATAGACTGGGAATATTGGCGCCACAGTG	675
Query	359	GGCCCGGAACCTGGAACCTCAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTCCGA	418
Sbjct	676	GGCCCGGAACCTGGAACCAAGGATATCTACAGACAGAAGTCAAGAACTTTATTCTGA	735
Query	419	TATGGGAA-AGAATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAG	477
Sbjct	736	TAT-GAAGAGAACATATCTGCTGCTGATATTGAATATTCAGCCAAAGGCACTTTTG-AG	793
Query	478	-AAAGTGCAAAAGCTTTTCATGAAGGAAACCATCAAATTTGGGAATTAAAGCGCCAGCCAAA	536
Sbjct	794	AAAAGTGCAAAAGCTTTTCATGGAGGAAACTATCAAATTTGGGAATTAAAGCAGCAACCAAG	853
Query	537	GGCCTTTGGGGTTATTATTATATCTGATTGCCCAATTTAAGCTTTATGCCCCAAAC	596
Sbjct	854	GGCCTTTGGGGTTATTATTATATCTGATTGCCCAATTTAATGTTTATGCCACAAAC	913
Query	597	TACT-CTGGGTCATGCCCAGAAGCAAGTCTTGAGGAACAATGAGCTCTCTGGCTCTG	655
Sbjct	914	TA-TACTGGGTCATGCCCAGAAGGGAAGTTTGAGGAACAATGAGCTCTCTGGCTCTG	972
Query	656	GAACAGCAGTGCTGCTTTATATCCCTTCTATCGGTGCTCT-GGAAATCCCTTGAGACAGTG	714
Sbjct	973	GAAACAGCAGTACAGCCCTGTATCTGCTGTGAGTAT-TAGGAAATCCCTTGAGACAGTG	1031
Query	715	AAAACATTTTGGCTTCTC-CAAATTTGGGTGCATGAATC-CATGAGGATCTCCACCAT	772
Sbjct	1032	AAAACACTTTGCATCTTCTACGA-TTTCGGGTGCGTGAATCAC-TGAGGATTTCCACCAT	1089
Query	773	GACATCTCATGATTATGCTCTGCCGTGATTGTCTACACA-AGGCTAGGG-TACAGAGAT	830
Sbjct	1090	GACATCAGGATTATGCTCTGCCGTGATTGTCTACACAG-CT-GGGCTACAAGAG	1147
Query	831	GAACCTTTATTTTCTCTTCTAAGCAAGATCTAGTCAGCACCATTAGGAGAAAGTGCTGCC	890

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Sbjct 1148 GAACCTTTACTTTTCTCTTCTAAGCAAGATCTAATTAGTAGCCATAGGAGAAAGTGCTGCG 1207
Query 891 TTGGGAGCTGCAGGCATTGTATTTTGGGGAGACATGAATTTAACTGCATCCAAGGCCAAC 950
Sbjct 1208 TTGGGAGCGCGCAGGCATTGTGTTTGGGGAGACATGAATTTAACTTCATCTGAGGAGAAAC 1267
Query 951 TGTAC-AAAGGTGAAGCAG-TTGTGAGTTCGTATTTAGGGAGCTACATAGCCAATGTGA 1008
Sbjct 1268 TGTACGAAA-GTAACC-GCTTTGTGAATCTGTATTTTGGCAGCTACATAATCAATGTGA 1325
Query 1009 CCAGAGCTGCTGAGGTATGCAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCATAAGGA 1068
Sbjct 1326 CCAGAGCAGCTGAGGTGTGCAGTCGTACCTTTGCAAGAATAATGGGAGGTGTGTACGGA 1385
Query 1069 AGATGTGGAACGC-GCCAGTTACCTTCACCTTGAAACCTCGCAAGTTACCACATAGAGGCC 1127
Sbjct 1386 AGACATGGAAAGCAGCTCA-TTACCTCCATTTGAAACCTCGCAAGTTACCACATAGAGGCC 1444
Query 1128 TCTGAGGACGGGGAGTTTACT-GTGAAAGGAAAAGCATCTGATACAGACCTGGCAGTGAT 1186
Sbjct 1445 TCTGAGGATGGGAATTCA-TAGTGAGGGGGAAGAGCATCAGACACTGACCTAGCTGTGAT 1503
Query 1187 GGCAGATACATTTTCT--GTCATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAA 1244
Sbjct 1504 GGCAGAGA-ATTT-CCTATGTCAGTGTATGAGGGATATGAGGGGGCTGACTGTAGAGAA 1561
Query 1245 AT 1246
Sbjct 1562 AT 1563

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>dbj|AK014599.1| **UEG** Mus musculus 0 day neonate skin cDNA, RIKEN full-length e library, clone:4632428M18 product:similar to HYALURONIDASE 4 [Homo sapiens], full insert sequence length=3255

GENE ID: 77042 Hyal4 | hyaluronoglucosaminidase 4 [Mus musculus]  
(Over 10 PubMed links)

Score = 1306 bits (707), Expect = 0.0  
Identities = 1085/1264 (85%), Gaps = 40/1264 (3%)  
Strand=Plus/Plus

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Query 3 CTAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGGAAATGCT 62
Sbjct 343 CTAAACCTGCCCCGACTTCCAGTTTATCAAAGGAAACCTTTTATGTGCTGCTTGGAAATGCT 402
Query 63 CCAACAGATCAGTGTTTGATAAAATATAATTTAAGACTAAATTTGAAAA-TGTTTCCTG- 120
Sbjct 403 CCAACAGACCTGTGTTTGTATAAAATATAATTTAACACTGAACCTT-AAAAGTGTTC-TAGA 460
Query 121 TGATTGGAAGCCCACTGGC-CAAGGCCAGGGGGCAAAATGTCACTATATTTTATGTCAAC 179
Sbjct 461 TGGTTGGAAGCCCTC-GGCTCAAAGACAGGGGGCAAAATGTGTTATATTTTATGCGCAAC 519
Query 180 AGATTGGGATACATTCCGTGGTATACATCACAAGGGGTCCCCATTAAATGGAGGTC-TCCC 238
Sbjct 520 AGATTGGGATATTACCCATGGTATACATCAGAAGGGGTACCATCAATGGTGGTCTTCCC 579
Query 239 ACAGAACATAAGTTTACAAGTACATCTGGAAA-AAGCTGACCAAGATATTAAATTATTACA 297
Sbjct 580 -CAAAACACAAGCTTTACAAGTACACCT-GAAAGGGGCTGGCCAGGATATTAAATTATTACA 637
Query 298 TCCCTGCTGAAGATTTTCAGTGGACTTGTCTGTTATAGATTGGGAATATTGGCGACCACAGT 357
Sbjct 638 TCCCTTCTGAAAAATTTTCAGTGGACTTGTCTGTTATAGACTGGGAATATTGGCGCCACAGT 697
Query 358 GGGCCCGGAACCTGGAACCTCAAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCG 417
Sbjct 698 GGGCCCGGAACCTGGAACCAAAAGGATATCTACAGACAGAAGTCAAGAACTCTTATTTCTG 757
Query 418 ATATGGGAA-AGAATGTATCAGCTACCGATATTGAATATTAGCCAAAGTGACCTTTTGAA 476
Sbjct 758 ATAT-GAAAGAGACATATCTGCTGTGATATTGAATATTACGCCAAGGCAACTTTTG-A 815

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Query	477	G-AAAGTGCAAAAGCTTTTCATGAAGGAAACCATAAATTTGGGAATTAAGAGCCGACCCAA	535
Sbjct	816	GAAAAGTGCAAAAGCTTTTCATGGAGGAAACTATCAAATTTGGGAAGTAAGAGCAGACCCAA	875
Query	536	AGGCCCTTTGGGGTTATTATTTATATCTGATTGCCACAATTTATAACGTTTATGCCCCAAA	595
Sbjct	876	GGGCCCTTTGGGGTTATTATTTATATCTGATTGCCACAATTTATAATGTTTATGCCACAAA	935
Query	596	CTACT-CTGGGTGATGCCCAGAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGCGCTCT	654
Sbjct	936	CTA-TACTGGGTGATGCCCAGAGAGGAAGTTTGAGGAACAATGAGCTCTCTTGCGCTCT	994
Query	655	GGAACAGCAGTGTCTCTTATATCCCTTCTATCGGTGTCT-GGAAATCCCTTGAGACAGT	713
Sbjct	995	GGAACAGCAGTACAGCCCTGTATCCTGCTGTCAAT-TAGGAATCCCTTGAGACAGT	1053
Query	714	GAAAACATTTTGCCTTCTC-CAAATTTCCGGTGATGAATC-CATGAGGATCTCCACCA	771
Sbjct	1054	GAAAACACTTTGCCTTCTCAGCA-TTTCGGGTGCGTGAATCAC-TGAGGATTTCCACCA	1111
Query	772	TGACATCTCATGATTATGCTCTGCCTGTATTTTGCTACACA-AGGCTAGGG-TACAGAGA	829
Sbjct	1112	TGACATCACAGGATTATGCTCTGCCTGTATTTTGCTACACACAG-CT-GGGCTACAAAGA	1169
Query	830	TGAACCTTTATTTTTC-TTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCTG	888
Sbjct	1170	GGAACTTTTACTTTTCCCTTT-TAAGCAAGATCTAATTAGTACCATAGGAGAAAGTGCTG	1228
Query	889	CCTTGGGAGCTGCAGGCATTGTTATTTGGGGAGACATGAATTTAACTGCATCCAAGGCCA	948
Sbjct	1229	CGTTGGGAGCGCAGGCATTGTTGTTTGGGGAGACATGAATTTAACTTCATCTGAGGACA	1288
Query	949	ACTGTAC-AAAGGTGAAGCAG-TTTGTGAGTTCGATTTTAGGGAGCTACATAGCCAAATGT	1006
Sbjct	1289	ACTGTACGAAAG-TGAACC-GCTTTGTGAATTCGATTTTGGCAGCTACATAATCAATGT	1346
Query	1007	GACCAGAGCTGCTGAGGTATGCAGCCTTCACTCTGCAGGAACAATGGCAGGTGCATAAG	1066
Sbjct	1347	GACCAGAGCAGCTGAGGTGTCAGTCGTCACTTTGCAAGAATAATGGGAGGTGTGTACG	1406
Query	1067	GAAGATGTGGAACGC-GCCAGTTACCTTCACTTGAACCTGCAAGTTACCACATAGAGG	1125
Sbjct	1407	GAAGACATGGAAGCAGCTCA-TTACCTCCATTTGAACCTGCAAGTTACCACATAGAGG	1465
Query	1126	CCTCTGAGGACGGGGAGTTTACT-GTGAAAGGAAAAGCATCTGATACAGACCTGGCAGTG	1184
Sbjct	1466	CCTCTGAGGATGGAGAATTCA-TAGTGAGGGGAAGAGCATCAGACACTGACCTAGCTGTG	1524
Query	1185	ATGGCAGATACATTTTCTCT--GTCATTGTATCAGGGATATGAAGGAGCTGATTGCAGAG	1242
Sbjct	1525	ATGGCAGAGA-ATTT-CCTATGTCACTGTATGAGGGATATGAGGGGGCTGACTGTAGAG	1582
Query	1243	AAAT	1246
Sbjct	1583	AAAT	1586

>ref|XM\_001370681.1| **G** PREDICTED: Monodelphis domestica similar to Hyaluronoglu  
 4 (LOC100017029), mRNA  
 Length=1446


GENE ID: 100017029 LOC100017029 | similar to Hyaluronogluccaminidase 4  
 [Monodelphis domestica]

Score = 1232 bits (667), Expect = 0.0  
 Identities = 1067/1261 (84%), Gaps = 24/1261 (1%)  
 Strand=Plus/Plus

Query	4	TAAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGGAAATGCTC	63
Sbjct	104	TAAAACCTGCACACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGGAAATGCTC	163
Query	64	CAACAGATCAGTGTTTGATAAAAATATAATTAA-GACTAAATTTGAAAATGTTTC-CTGT	121
Sbjct	164	CAACAGATCAGTGTTTCAACAAAGTATATATAATG-CTGAATTTAAAAATGTTTCACA-T	221

Query	122	GATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAAATGTCACATATTTTATGTCAACAG	181
Sbjct	222	CATTGGCAGTCCATTGGCCAAGGCCAGAGGGGCAAAATGTTACCATATTTTATGTCAATAG	281
Query	182	ATTGGGATACATTCCTGGGTATACATCACAAAGGGTCCCCATTAAATGGAGGTCT-CCCAC	240
Sbjct	282	ATTGGGATATTTATCCTGGGTATACATCACAAAGGAGTTCCTTTAATATGGGGGCTTCCC-C	340
Query	241	AGAACATAAGTTTACAAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACATCC	300
Sbjct	341	AGAACTTTAGTTTGCAAGCCCATCTGGAAAAAGCTGGCCAAAGACATCAATTAATTATATTC	400
Query	301	CTGCTGAAGATTTTCAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGTGGG	360
Sbjct	401	CAGCTGAGGATTTTCAGTGGACTTGCTGTCTAGACTGGGAATATTGGAGACCTCAATGGG	460
Query	361	CCCGGAAC TGGAAC TCAAAAGATGTTTACAGACAGAAAGTCAAGAAAGCTTAATTTCCGATA	420
Sbjct	461	CACGGAATTGGAAACACAAAGATGTATACAGGCAGAAAGTCAAGAAAGCTTAATTTCTGA-A	519
Query	421	TGGGAAAG--AATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAGA	478
Sbjct	520	-GTAAAGTGAACATGTCAGCTAGTGAATTTGAATATTTAGCCAAATTTCTTTTGGGA	578
Query	479	AAGTGAAGAAAGCTTTCATGAAGGAAACCATCAAATTGGGAATTAAGA-GCCGACCCAAAG	537
Sbjct	579	AAGTGAAGAAAGCTTTCATGAAGGAAACCATCCAGTTGGGAATTC-GAAGTCGCCCCAGGG	637
Query	538	GCCTTTGGGGTTATTAATTTATATCCTGATTGCCACAATTTAAGCTTTATGCCCCAAACT	597
Sbjct	638	GTCTTTGGGGTTACTAATTTATATCCTGATTGTACAATTTACAACATTTATGACCAAAATT	697
Query	598	ACTCTGGGTCATGCCAGAGACGAAGTCTTGAGGAACAAATGAGCTCTCTTGCTCTGGA	657
Sbjct	698	ACACTGGTTTCATGTCAGAAAGTGAAGTTTGAGGAACAAATGAGCTTCTCTTGCTTTGGA	757
Query	658	ACAGCAGTGTCTGCTTTATATCCTTCTATCGGTGTCTGGAATCCCTTTGGAGA-CAGTGAA	716
Sbjct	758	ACAGCAGTGTCTGCTTTATATCCTTCCATTTGGAGTCAAGAAATCTTTTGG-GAAGCAGTGA	816
Query	717	AACATTTTGGCTTCTC-C-CAAATTTGCGGTGCATGAATCCATGAGGATCTCCACCATGAC	775
Sbjct	817	AACATTTTACGCTTCTCTCAG-TTTAGGTAATGAATCAATGCGGATTTCTACCATGAC	875
Query	776	ATCTCATGATTATGCTCTGCCTGTATTTGTCTACCAAGGCTAGGG-TACAGAGATGAAC	834
Sbjct	876	ATCTCATGATTATGCTCTGCCTGTATTTGTCTATACAAGGCT-GGGATACAGAGATGAGC	934
Query	835	CTTTAT-TTTTCCCTTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCTGCCTTG	893
Sbjct	935	CATTATATTTTC-TTCCAAAGCAAGATCTAATTAGTACCATAGGAGAAAGTGCTGCCTTG	993
Query	894	GGAGCTGCAGGCATTGTTATTTGGGGAGACATGAATTTAACTGCATCCAAGGCCAACTGT	953
Sbjct	994	GGAGCTGCAGGCATTGTTATTTGGGGAGACATGAATTTAACTTCCCTGAGGGCAACTGT	1053
Query	954	ACAAAGGTGAAGCAGTTTGTGAGTTCTGATTAGGGAGCTACATAGCCAAATGTGACCAGA	1013
Sbjct	1054	ACAAAGGTGAAGCAGTTTGTGACTTCTGATCTAGGGAGCTACATGTTAATGTGACCAAA	1113
Query	1014	GCTGCTGAGGTATGACGCCTTCACTCTGAGGAAACATGGCAGGTGCATAAGGAAGATG	1073
Sbjct	1114	GCAGCTGAAGATGACGACGAGCTCTCTGTAGGAATAATGGAAGATGTGTAAGAAAAATC	1173
Query	1074	TGGAACGCGCCAG-TTACCTTCACTTGAACCCCTG-CAAGTTACCACATAGAGGCCCTCTG	1131
Sbjct	1174	TGGAAGGCGGC-AGATTATCTCCACTTGAACCCCTGACAACTG-CCAGATAGAGGTCTCTG	1231
Query	1132	AGSACGGGGAGTTTACTGTGAAAGGAAAGCATCTGTATACAGACCTGGCAGTGTATGGCAG	1191
Sbjct	1232	ATGATGGAGACTTTGCTGTGAAAGGAGAAACCTCTGATTGAGACTTGAAGTGTATGGCAG	1291
Query	1192	ATACATTTTCTCTGTCATTGTTATCAGGGATATGAAGGAGCTGATTGCGAGAAATAAGA	1251
Sbjct	1292	AGAGATTTTCTTGTCTATTGTTATCAGGGATATGGAGGAAAGGATTGCGAGGAAATGAAGA	1351

Query 1252 C 1252  
Sbjct 1352 C 1352

>ref|XM\_001062033.1|  PREDICTED: Rattus norvegicus hyaluronoglucosaminidase 4 (mRNA)  
Length=1446

GENE ID: 404783 Hyal4 | hyaluronoglucosaminidase 4 [Rattus norvegicus]  
(10 or fewer PubMed links)

Score = 1212 bits (656), Expect = 0.0  
Identities = 1067/1262 (84%), Gaps = 42/1262 (3%)  
Strand=Plus/Plus

Query	3	CTAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGGAAATGCT	62
Sbjct	103	CTAAACCTGCTCGACTTCCAGTTTATCAAAGGAAACCTTTTATAGCTGCTTGGAAATGCT	162
Query	63	CCAACAGATCAGTGTGGATAAAATATAATTAAAG-CTAAATTTGAAAA-TGTTTCCTG	120
Sbjct	163	CCAACAGACCTGTGTGGATAAAATATAATTG-GCAGTGAACCTT-AAAAGTGTTC-A-G	219
Query	121	-TGATTGGAAGCCCACTGGC-CAAGGCCAGGGGGCAAAATGTCACTATATTTATGTCAA	178
Sbjct	220	ATGGTGGGAAGCCCTC-GGCTCAAAGCAGGAGGCCAAATGTGTATATTTATGCCAA	278
Query	179	CAGATTGGGATACT-ATCCGTGGTATACATCACAAGGGGTCCCCATTAATGGAGGTCT-C	236
Sbjct	279	CAAAATGGGAT-CTTACCCATGGTATACATCAGAAGGGGTACCCATCAATGGTGGTCTTC	337
Query	237	CCACAGAACATAAGTTTACAAGTACATCTGAAAAAGCTGACCAAGATATTAATTATTAC	296
Sbjct	338	CC-CAAAACACAGACTTACAGGTACACCTGGAAAAAGGCTTACCAGGATATTAATTATTAC	396
Query	297	ATCCCTGCTGAAGATTTTCAAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGCCACAG	356
Sbjct	397	ATCCCTTCTGAAAAATTTCAAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGCCACAG	456
Query	357	TGGGCCCGGAACCTGGAACCTCAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTC	416
Sbjct	457	TGGGCCCGGAACCTGGAACCAAGGATATCTACAGACAGAAGTCAAGAACTCTTATTCT	516
Query	417	GATATG--GGAAAGAAATGTATC-AGCTACCGATATTGAATATTTAGCCAAAGTGACCTTT	473
Sbjct	517	GATATGAAGGA--GAACATATCCA-CTGCTGATATTGAATATTTAGCCAAAGCAACTTTT	573
Query	474	GAAGAAA-GTGCAAAAGCTTTCATGAAGGAAACCATCAAAATGGGAATTAAGAGCCGACC	532
Sbjct	574	GA-GAAAGTGCAAAGCTTTCATGGAGGAAACATATCAAAATGGGAATTAAGAGCAGACC	632
Query	533	CAAGGCGCTTTGGGGTTATTATTATATCTGATTGCGCACAAATTATAACGTTTATGCCCC	592
Sbjct	633	CAAGGCGCTTTGGGGTTATTACTTGTATCTGACTGCCACAAATTACAATTTTATGCTAC	692
Query	593	AAACTACT-CTGGGTCATGCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGC	651
Sbjct	693	AAACTA-TACCGGTCATGCCAGAAGAGGAAGTTTGAGGAACAATGACCTCTCTTGGC	751
Query	652	TCTGGAACAGCAGTGTGCTTTATATCTTCTATCGGTGTCT-GGAAATCCCTTGGAGAC	710
Sbjct	752	TCTGGAACAGCAGTACTGCTCTGTATCTGCTGTAGTAT-TAGGAATCCCTTGCAGAC	810
Query	711	AGTGAACCAATTTTGGCGCTTCTC-CAAATTTGGGTGTCATGAATC-CATGAGGATCTCCA	768
Sbjct	811	AGTGAACCAATTTTGGCACTTCTCAAA-TTTCGGGTGCGTGAATCAC-TGAGGATCTCTA	868
Query	769	CCATGACATCTCATGATTATGCTCTGCTGTATTTGCTACACAAGGCTAGGG-TACAGA	827
Sbjct	869	CTATGACATCATGATTATGCTCTGCTGCTGTATTTGCTACACAGGCT-GGGCTACAAA	927
Query	828	GATGAACCTTTATTTTCTTTCTTAAGCAAGATCTAGTCAGCACCATTAGGAGAAAGTGCT	887

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Sbjct  928  GAGGAACCTTTGCTTTTCTCTTCTAAGCAAGATCTAATTAGTACCATAGGAGAAAGTGCT  987
Query   888  GCCTTGGGAGCTGCAGGCATTTGTTATTTGGGGAGACATGAATTTAACTGCATCCAAGGCC  947
Sbjct  988  GCGTTGGGAGCTGCAGGCATTTGTTGTTGGGGAGACATGAATTTAACTTCATCTGCGGAG  1047
Query   948  AACTGTACAAAGGTGAAGCAG-TTGTGAGTCTGAATTTAGGGAGCTACATAGCCAATGT  1006
Sbjct  1048  AACTGTACAAAGGTGAACC-GCTTTGTGAACCTGTGATTTTGGTAGCTACGTAATCAATGT  1106
Query  1007  GACCAGAGCTGCTGAGGATATGCAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCATAAG  1066
Sbjct  1107  GACCACAGCAGCTGAAGTGTGCAGTCTGTCATCTTGCAGAAACAATGGGAGGTGTGCACG  1166
Query  1067  GAAGATGTGGAACGC-GCCCAGTTACCTTCACCTGAACCTCGCAAGTTACACATAGAGG  1125
Sbjct  1167  GAAGACATGGAAGCAGCTCA-TTACCTCCACTTGAACCTCGCAGTTACCAATAGAGG  1225
Query  1126  CCTCTG-AGGACGGGGAGTT--TACTGTGAAAGGAAAGCATCTGATACAGACCTGGCAG  1182
Sbjct  1226  CCTCTGCAG-ATAGAGAATTCGTA--GTGAAGGGAGAGAGCGTCAGATGCTGACCTAGCCG  1282
Query  1183  TGATGGCAGATACATTTTCC-TGTCATTGTTATCAGGGATATGAAGGAGCTGATTGCAGA  1241
Sbjct  1283  CCATGGCAGAGA-ATTTTCTATGTCTACTGTTATGAGGGCTATGAGGGGGCTGACTGTAGA  1341
Query  1242  GA  1243
Sbjct  1342  GA  1343

```

>ref|XM\_578235.1| **UG** PREDICTED: Rattus norvegicus hyaluronoglucosaminidase 4 (H mRNA)  
Length=1446

GENE ID: 404783 Hyal4 | hyaluronoglucosaminidase 4 [Rattus norvegicus]  
(10 or fewer PubMed links)

Score = 1212 bits (656), Expect = 0.0  
Identities = 1067/1262 (84%), Gaps = 42/1262 (3%)  
Strand=Plus/Plus

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Query   3  CTAAAACTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGAATGCT  62
Sbjct  103  CTAAAACTGCTCGACTTCCAGTTTATCAAAGGAAACCTTTTATAGCTGCTTGAATGCT  162
Query   63  CCAACAGATCAGTGTGTTGATAAAATATAATTTAAG-ACTAAATTTGAAAA-TGTTTCTG  120
Sbjct  163  CCAACAGACCTGTGTTTGATAAAATATAATTTG-GCAGTGAACCTT-AAAAGTGTTCAG  219
Query  121  -TGATTGGAAGCCCACTGGC-CAAGGCCAGGGGGCAAAATGTCCTATATTTTATGTCAA  178
Sbjct  220  ATGGTTGGAAGCCCTC-GGCTCAAAGACAGGAGGCAAAATGTTGTTATATTTATGCCAA  278
Query  179  CAGATTGGGATACT-ATCCGTGGTATACATCACAAGGGGTCCCAATTAATGAGGTCT-C  236
Sbjct  279  CAAATTGGGAT-CITACCCATGGTATACATCAGAAGGGGTACCCATCAATGTTGTTCTC  337
Query  237  CCACAGAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTAATAC  296
Sbjct  338  CC-CAAAACAACAGCTTACAGGTACACTTGGAAAAAGGCTTACCAAGATATTAATTAATAC  396
Query  297  ATCCCTGCTGAAGATTTTCAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCAAG  356
Sbjct  397  ATCCCTTCTGAAAAATTTTCAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGCCACAG  456
Query  357  TGGGCCCCGAACTGGAACCTCAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTTCC  416
Sbjct  457  TGGGCCCCGAACTGGAACACCAAGGATATCTACAGACAGAAGTCAAGAACTCTTATTTCT  516
Query  417  GATATG--GGAAAGAAATGTATC-AGCTACCGATATTGAATATTTAGCCAAAGTGACCTTT  473
Sbjct  517  GATATGAAGGA--GAACATATCCA-CTGCTGATATTGAATATTTAGCCAAAGCAACTTTT  573
Query  474  GAAGAAA-GTGCAAAAGCTTTTCATGAAGGAAACCATCAAATTGGGAATTAAAGACCCGACC  532

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Sbjct 574 GA-GAAAAGTGCAAAAGCTTTCATGGAGGAAACTATCAAATTGGGAATTAAAGAGCAGACC 632
Query 533 CAAAGGCGCTTTGGGGTTATTATTTATATCCTGATTGCCACAATTATAACGTTTATGCCCC 592
Sbjct 633 CAAGGGCTTTTGGGGTTATTACTTGTATCCTGACTGCCACAATTACAAATTTTATGCTAC 692
Query 593 AAACCTACT-CTGGGTCATGCCAGAGCAAGCTCTTGAGGAACAATGAGCTCTCTTGGC 651
Sbjct 693 AAACCTA-TACCGGGTCATGCCAGAGGAAAGTTTTGAGGAACAATGAGCTCTCTTGGC 751
Query 652 TCTGGAACAGCAGTGTCTGCTTTATATCCTTCTATCGGTGTCT-GGAAATCCCTTGGAGAC 710
Sbjct 752 TCTGGAACAGCAGTGTCTGCTTCTATCCTGTCTGTAGTAT-TAGGAATCCCTTGCAGAC 810
Query 711 AGTGAAACATCTTTTGGCGCTTCTC-CAAATTTGGGGTGCATGAATC-CATGAGGATCTCCA 768
Sbjct 811 AGTGAAATACCTTTGCACCTTCTCACA-TTTCGGGTGCGTGAATCAC-TGAGGATCTCTA 868
Query 769 CCATGACATCTCATGATTATGCTCTGCCTGTATTTGTCTACACAAGGCTAGGG-TACAGA 827
Sbjct 869 CTATGACATCAGATGATTATGCTCTGCCCGTATTTGTCTACACAGGCT-GGGCTACAAA 927
Query 828 GATGAACCTTTTATTTTCCCTTTCCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCT 887
Sbjct 928 GAGGAACCTTTGCTTTTCCCTTTCCTAAGCAAGATCTAATTAGTACCATAGGAGAAAGTGCT 987
Query 888 GCCTTGGGAGCTGCAGGCATGTATTATTGGGGAGACATGAATTTAACTGCATCCAAGGCC 947
Sbjct 988 GCGTTGGGAGCTGCAGGCATGTATTATTGGGGAGACATGAATTTAACTTCATCTGCGGAG 1047
Query 948 AACTGTACAAAGGTGAAGCAG-TTGTGTAGTTCTGATTTTAGGAGCTACATAGCCAAATGT 1006
Sbjct 1048 AACTGTACAAAGGTGAACC-GCTTTGTGAATCTGATTTTGGTAGCTACGTAAATCAATGT 1106
Query 1007 GACCAGAGCTGTCTGAGGTATGCAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCATAAG 1066
Sbjct 1107 GACCAGAGCAGCTGAAGTGTGCAGTCGTATCTTTGCAAGAACAAATGGGAGGTGTGCACG 1166
Query 1067 GAAGATGTGGAACGC-GCCAGTTACCTTCACTTGAACCTCGCAAGTTACCACATAGAGG 1125
Sbjct 1167 GAAGACATGGAAAGCAGCTCA-TTACCTCCACTTGAACCTCGCAGTTTACCACATAGAGG 1225
Query 1126 CCTCTG-AGGACGGGGAGTT--TACTGTGAAAGGAAAGCATCTGATACAGACCTGGCAG 1182
Sbjct 1226 CCTCTGCAG-ATAGAGAATTCGTA--GTGAAGGGAAGAGCGCTAGATGCTGACCTAGCCG 1282
Query 1183 TGATGGCAGATACATTTTCC-TGTCATTGTTATCAGGGATATGAAGAGCTGATTGCAGA 1241
Sbjct 1283 CCATGGCAGAGA-ATTTTCTATGTCACGTATTATGAGGGCTATGAGGGGCTGACTGTAGA 1341
Query 1242 GA 1243
Sbjct 1342 GA 1343

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>emb|CU467663.10| **D** Pig DNA sequence from clone CH242-113A4 on chromosome 18, co  
sequence  
Length=162313

Sort alignments for this  
E value Score Perce  
Query start position

Score = 1136 bits (615), Expect = 0.0  
Identities = 780/859 (90%), Gaps = 14/859 (1%)  
Strand=Plus/Minus

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Query 3 CTAACACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGGAAATGCT 62
Sbjct 147609 CTAACACCTGCCCCGACTTCCAGTTTACCAAGGAAACCTTTTATAGCTGCTTGGAAATGCT 1475
Query 63 CCAACAGATCAGTGTTTGATAAAAATATAATTTAAGACTAAATTTGAAAAATGTTTCCTGTG 122
Sbjct 147549 CCAACAGATCAGTGTTTGATAAAAATATAATTTAAGACTAAATTTGAAAAATGTTTCAGTA 1474

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Query 123      ATTGGAAGCCCACTGGCCAAGGCCAGGGGCAAAATGTCACTATATTTTATGTCAACAGA 182
Sbjct 147489   ATTGGAAGTCCACTGGCCAGGGCCAGGGGCAAAATGTCACTATATTTTATGTCAACAGA 1474

Query 183      TTGGGATACATCCCGTGGTATACATCACAAGGG -GTCCCATTAATGGAGGTCTCCCA 241
Sbjct 147429   CTGGGATACTACTCTTGGTATACAGC -CCAGGGATTCCTCATTAATGGGGGTCTCCCCA 1473

Query 242      GAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATTAATTAATTACATCCC 301
Sbjct 147370   GAACATAAGTCTGCAGGTACATCTGGAAAAAGCAGACCAAGACATTAATTAATTACATCCC 1473

Query 302      TGCTGAAGATTTCAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGTGGGC 361
Sbjct 147310   TTCTGAAGATTTCAGTGGACTTGCTGTTATAGACTGGGAATATTGGCGACCCACAGTGGGC 1472

Query 362      CCGGAAC TGGAAC TCAAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCGATAT 421
Sbjct 147250   CAGGAAC TGGAAC CAAAAAGATGTCTACAGACAGAAGTCAAGAAAGCTTATTTCTGAGCT 1471

Query 422      GGGAA -AGAATGTAT -CAGCT -ACCGATATTGAATATTTAGCCAAAGTGACCTTT -GAAG 477
Sbjct 147190   -GCAAGAGAATGTGTCCA - -TGGCTGATATTGAATATTAGCCAAA -ACRACTTTGAGG 1471

Query 478      AAAGTGCAAAAGCTTTCATGAAGGAACCATCAAATTTGGGAATTAAAGAGCCGACCCAAAG 537
Sbjct 147134   AAAGTGCAAAAGCTTTCATGAAGGAACCATCGAATTTGGGAATTAAAGAGCAGACCCAAAG 1470

Query 538      GCCTTTGGGGTTATTATTATATCCTGATTGCCACAATTATAACGTTTATGCCCCAAACT 597
Sbjct 147074   GCCTTTGGGGTTACTATTATATCCTGACTGCCACAATTATAATGTTTATGCCCCAAACT 1470

Query 598      ACT -CTGGGTCATGCCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTGG 656
Sbjct 147014   A -TACGGGTCCTTGCCCAGAAGAAGAAGTTTGAGGAACAACGAGCTCTCTTGGCTCTGG 1469

Query 657      AACAGCAGTGCTGCTTTATATCCTTCTATCCGTGTCTGGAAATCCCTTGGAGACAGTGAA 716
Sbjct 146955   AACAGCAGTGCTGCTTTATATCCTTCTATCAGCGCTCAGGAAATCCCTTGGGAGACAGTGAA 1468

Query 717      AACATTTTGGCCTTCTC -CAAATTTGGGTGCATGAATCCATGAGGATCTCCACCATGAC 775
Sbjct 146895   AACACTTTGCGTTTCTCACA -TTTCGGGTGCATGAATCCATGAGGATCTCCACCGTGAC 1468

Query 776      ATCTCATGATTATGCTCTGCCTGTATTGTCTACACAAGGCTAGGGTACAGAGATGAACC 835
Sbjct 146836   ATCCCATGGTATTGCTCTGCCTGTGTTGTCTACACAAGGCTAGGCTACAGAGACCAACC 1467

Query 836      TTTATTTTTCCTTTCTAAG 854
Sbjct 146776   TCTGTTTTTCTTTCTAAG 146758

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Score = 381 bits (206), Expect = 4e-102  
 Identities = 294/336 (87%), Gaps = 7/336 (2%)  
 Strand=Plus/Minus

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Query 939      TCCAAGGCCCACTGTACAAAGGTGAAGCAGTTTGTGAGTTCGTGATTTAGGGA -GCTACAT 997
Sbjct 140425   TCC -AGGGCAACTGTACAAAGGTGAAGCAGTTTGTGAGTTCGTGACCTA -GGACACTACGT 1403

Query 998      AGCCCAATGTGACCAGAGCTGCTGAGGTATGCAGCCCTCACCTCTGCAGGAACAATGGCAG 1057
Sbjct 140367   AGTGAACGTGACAGAGCCGCTGAGGTGTGCAGCCCTCACCTCTGCAGGAATAACGGGAG 1403

Query 1058     GTGCATAAGGAAGATGTGGAACGCGCCAG -TTACCTTCACCTGAACCCCTGCAAGTTACC 1116
Sbjct 140307   ATGCCTAAGGAAGGTGTGGAAAGC -TCCGATTACCTTCACCTGAACCCCTGCAAGTTACC 1402

Query 1117     ACATAGAGGCCCTCTGAGGACGGGGAGTTTACTGTGAAAGGAAAAGCATCTGATACAGACC 1176
Sbjct 140248   GCATAGAGGCCCTCTGAGGATGGAGAATTACTGTGAAAGGAAGAGCATCTGATAGAGACC 1401

Query 1177     TGGCAGTGATGCGAGATACATTTTCTGTCATTGTTATCAGGGATATGAA -GGAGCTGAT 1235

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Sbjct 140188 TGGCAGTGCTGGTGGAGAGATCTCTGTGTCATTGTTATCAGGGATATGAAGGA-CTGAT 1401  
 Query 1236 TGCAGAGAAAATAAGACGGCTGATGGCTGCTCTGGG 1271  
 Sbjct 140129 TGCAGAGAAATGAAGAGGGCAGATGGCTGCTCTGGG 140094

Score = 113 bits (61), Expect = 2e-21  
 Identities = 83/93 (89%), Gaps = 3/93 (3%)  
 Strand=Plus/Minus

Query 849 TCTAAGCAAGATC-TAGTCAGCACCATAGGAGAAAGTGCTGCCTTGGGAGCTGCAGGCAT 907  
 Sbjct 142382 TCT-AGCAAGATCTTA-TCAGTACTATTGGAGAAAGTGCTGCCTTGGGTGCTGCCGGCTT 1423  
 Query 908 TGTATTATTGGGGAGACATGAATTTAACTGCATC 940  
 Sbjct 142324 TGTATTATTGGGGAGACATGAATTTAACTTCATC 142292

>gb|AC130215.3| **D** Mus musculus BAC clone RP23-286E1 from 6, complete sequence  
 Length=168515

Sort alignments for this  
 E value Score Percen  
 Query start position

Score = 976 bits (528), Expect = 0.0  
 Identities = 756/864 (87%), Gaps = 24/864 (2%)  
 Strand=Plus/Plus

Query 3 CTAAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGGAAATGCT 62  
 Sbjct 106524 CTAAAACCTGCCCGACTTCCAGTTTATCAAAGGAAACCTTTTATTGCTGCTTGGAAATGCT 1065  
 Query 63 CCAACAGATCAGTGTTTGATAAAATATAATTTAAGACTAAATTTGAAAA-TGTTTCCTG- 120  
 Sbjct 106584 CCAACAGACCTGTGTTTGATAAAATATAATTTAACACTGAACCTT-AAAAGTGTTT-CAGA 1066  
 Query 121 TGATTGGAAGCCCATCGGC-CAAGGCCAGGGGGCAAAATGTCACTATATTTTATGTCAAC 179  
 Sbjct 106642 TGGTGTGAAGCCCTC-GGCTCAAAGACAGGGGGCAAAATGTTGTTATATTTTATGCCAAC 1067  
 Query 180 AGATTGGGATACTATCCGTGGTATACATCACAAGGGGTCCCCATTAATGGAGGTC-TCCC 238  
 Sbjct 106701 AGATTGGGATATTACCATGGTATACATCAGAAGGGGTACCCATCAATGGTGGTCTTCCC 1067  
 Query 239 ACAGAACATAAGTTTACAAGTACATCTGGAAGAAAGCTGACCAAGATATTAATTTATACAT 298  
 Sbjct 106761 -CAAAACACAAGCTTACAAGTACACTGAAAAAGAGCTGCCAGGATATTAATTTATACAT 1068  
 Query 299 CCCTGCTGAAGATTTTCACTGGACTTGCTGTTTATAGATTGGGAATATTGGCGACCACAGTG 358  
 Sbjct 106820 CCCTTCTGAAAAATTTCACTGGACTTGCTGTTTATAGACTGGGAATATTGGCGCCACAGTG 1068  
 Query 359 GGCCCGGAACCTGGAACCTCAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCGA 418  
 Sbjct 106880 GGCCCGGAACCTGGAACACAAAGGATATCTACAGACAGAAGTCAAGAACTCTTATTTCTGA 1069  
 Query 419 TATGGGAA-AGAATGTATCAGCTACCGATATTGAATATTAGCCAAAGTGACCTTTGAAG 477  
 Sbjct 106940 TAT-GAAAGAGAACATATCTGCTGTGATATTGAATATTACGCCAAGGCAACTTTTG-AG 1069  
 Query 478 -AAAGTGCAAAAGCTTTTCATGAAGGAAACCATCAAATTTGGGAATTAAGAGCCGACCCAAA 536  
 Sbjct 106998 AAAAGTGCAAAAGCTTTTCATGGAGGAAACATCAAATTTGGGAAGTAAGAGCAGACCCAAG 1070  
 Query 537 GGCCTTTGGGGTTATTTATTTATATCCTGATTGCCACAATTATAACGTTTATGCCCAAAAC 596  
 Sbjct 107058 GGCCTTTGGGGTTATTTATTTATATCCTGATTGCCACAATTAATATGTTTATGCCACAAC 1071  
 Query 597 TACT-CTGGGTGATGCCAGAGACGAAGTCTTGAGGAACAAATGAGCTCTCTTGCGCTCTG 655  
 Sbjct 107118 TA-TACTGGGTGATGCCAGAGAGGAAGTTTGGAGGAACAAATGAGCTCTCTTGCGCTCTG 1071

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Query 656      GAACAGCAGTGTGCTTTATATCCTTCTATCGGTGTCT-GGAAATCCCTTGGAGACAGTG 714
Sbjct 107177   GAACAGCAGTACAGCCCTGTATCTGCTGTCTAGTAT-TAGGAAATCCCTTGCAGACAGTG 1072

Query 715      AAAACATTTTGGCGTTCTC-CAAATTTTCGGGTGCATGAATC-CATGAGGATCTCCACCAT 772
Sbjct 107236   AAAACACTTTGCACTTCTCACGA-TTTTCGGGTGCGTGAATCAC-TGAGGATTTCCACCAT 1072

Query 773      GACATCTCATGATTATGCTCTGCCTGTATTTGTCTACACA-AGGCTAGGG-TACAGAGAT 830
Sbjct 107294   GACATCA CAGGATTATGCTCTGCCTGTATTTGTCTACACACAG-CT-GGGCTACAAAGAG 1073

Query 831      GAACCTTTATTTTTCCTTTCTAAG 854
Sbjct 107352   GAACCTTTACTTTTTCCTTTCTAAG 107375

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Score = 254 bits (137), Expect = 9e-64  
 Identities = 251/305 (82%), Gaps = 12/305 (3%)  
 Strand=Plus/Plus

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Query 948      AACTGTAC-AAAGGTGAAGCAG-TTTGTGAGTCTGATTTTAGGAGCTACATAGCCAATG 1005
Sbjct 116333   AACTGTACGAAA-GTGAA-CCGCTTTGTGAATCTGATTTTGGCAGCTACATAATCAATG 1163

Query 1006     TGACCAGAGCTGCTGAGGTATGCAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCATAA 1065
Sbjct 116391   TGACCAGAGCAGCTGAGGTGTGCAGTCGTCACTTTGCAAGAATAATGGGAGGTGTGTAC 1164

Query 1066     GGAAGATGTGGAACGC-GCCAGTTACCTTCACTTGAACCTTGCAAGTTACCACATAGAG 1124
Sbjct 116451   GGAAGACATGGAAGACAGCTCA-TTACCTCCATTGGAACCTTGCAAGTTACCACATAGAG 1165

Query 1125     GCCTCTGAGGACGGGGAGTTTACT-GTGAAAGGAAAAGCATCTGATACAGACCTGGCAGT 1183
Sbjct 116510   GCCTCTGAGGATGGAGAATTCA-TAGTGAGGGGAAGAGCATCAGACACTGACCTAGCTGT 1165

Query 1184     GATGGCAGATACATTTTCTCT--GTCATTGTTATCAGGGATATGAAGGAGCTGATTGCAGA 1241
Sbjct 116569   GATGGCAGAGA-ATTT-CCTATGTCACGTGTTATGAGGGATATGAGGGGGCTGACTGTAGA 1166

Query 1242     GAAAT 1246
Sbjct 116627   GAAAT 116631

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>ref|XM\_854096.1| **UEG** PREDICTED: Canis familiaris similar to hyaluronoglucosaminidase 4, transcript variant 3 (LOC475212), mRNA  
 Length=1060

**GENE ID: 475212 HYAL4** | hyaluronoglucosaminidase 4 [Canis lupus familiaris]

Score = 475 bits (257), Expect = 2e-130  
 Identities = 372/427 (87%), Gaps = 9/427 (2%)  
 Strand=Plus/Plus

```

Query 849      TCTAAGCAAGATCTAGTCAGCACCATTAGGAGAAAGTGCTGCCTTGGGAGCTGCAGGCATT 908
Sbjct 249      TCT-AGCAAGATCTAATTCAGTACTATTGGAGAAAGTGCTGCCTTGGGAGCTGCAGGCATT 307

Query 909      GTTATTTTGGGGAGACATGAATTTAACTGCATCCAAGGCCAACTGTACAAAGGTGAAGCAG 968
Sbjct 308      GTTATCTGGGGAGACATGAATTTAACTTCATCTGAGGGCAACTGTACAAAGGTGAAGCAG 367

Query 969      TTTGTGAGTCTGATTTTAGGG-AGCTACATAGCCCAATGTGACCAGAGCTGTCTGAGGTATG 1027
Sbjct 368      TATGTGAGTCTGACTTTAGGACA-CTACATAGTCAATGTGACCAGAGCGGCTGAGGTGTG 426

Query 1028     CAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCATAAGGAAGATGTGGAACGCGCCC-A 1086
Sbjct 427     CAGCCTTCACCTGTGCAGGAGTAATGGGAGATGCATAAGGAAGGTATGGAAGAGTCTCTTA 486

Query 1087     GTTACCTTCACTTGAACCTTGCAAGTTACCACATAGAGGCCTCTGAGGACGGGGAGTTTA 1146
Sbjct 487     -TTACCTGCACCTGAAACCTTGCAAGTTACCACATAGAGGCCTCCAAGGATGGAGAAATTTA 545

```

```

Query 1147 CTGTGAAAGGAAAAGCATCTGATACAGACCTGGCAGTGTGGCAG-ATACA-TTTTCCTG 1204
           |||
Sbjct 546 TTGTGAAAGGAAAAGCATCTGATATGGACCTGGAAGCGTTGG-AGGAGA-AGTTTTCCTG 603
           |||

Query 1205 TCATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAATAAAGACGGCTGATGGCTG 1264
           |||
Sbjct 604 TCATTGTTATCAGGGATACGAAGGAGCCGACTGTAGAGGAACAAGACGGCTGACGGCTG 663
           |||

Query 1265 CTCTGGG 1271
           |||
Sbjct 664 CTCTGGG 670
           |||

```

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environment samples or phase 0, 1 or 2 HTGS sequences)

Posted date: Jun 23, 2008 5:48 PM

Number of letters in database: -1,684,036,029

Number of sequences in database: 6,953,186

```

Lambda      K      H
1.33      0.621      1.12

```

Gapped

```

Lambda      K      H
1.33      0.621      1.12

```

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 0, Extension: 0

Number of Sequences: 6953186

Number of Hits to DB: 3393652

Number of extensions: 1

Number of successful extensions: 1

Number of sequences better than 10: 1

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 1271

Length of database: 24085767743

Length adjustment: 33

Effective length of query: 1238

Effective length of database: 23856312605

Effective search space: 29534115004990

Effective search space used: 29534115004990

A: 0

X1: 15 (28.8 bits)

X2: 32 (59.1 bits)

X3: 54 (99.7 bits)

S1: 15 (28.8 bits)

S2: 22 (41.7 bits)